

STIC Search Report

STIC Database Tracking Number

TO: Ginny Portner

Location: REM-3B02&3C4C70

Art Unit: 1645

Monday, April 25, 2005

Case Serial Number: 10/039183

From: Deirdre Arnold

Location: Biotech-Chem Library

REM 1A64

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards, Deirdre Arnold



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CAO 1360 SBO Page 3

US-10-039-:	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	FEATURES BOURCE ORIGIN	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	RESULT 3 BD082346 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	B 왕	B 8	B 8	B 8	망 왕	Q Q
183A-2 (1-299)	Scores: milarity: Similarity: h:	PC G01N CC Stra CC Topo FH Key	CCINS SECR JAN GENOME JP 2001 27-NOV- 31-MAR- HAROLD HAROLD ILLER, AMAL AL A01N43/ A61K39/	Viruses; dsDNA 1 (bases 1 to Kleanthous,H., 76 kDa, 32 kDa corresponding 1 Patent: JP 2003	BD082346 76 kDa, 32 kDa, and 50 corresponding polynucle BD082346 BD082346.1 GI:22627956 JP 2001523954-A/53. Mastadenovirus Mastadenovirus	281 ArgMetAsnGlı 	261 ThrTyrGluGli 886 ACTTATGAACA	241 LysThrGluph	221 ProAspPheSe	201 AsnSerLysAsı 706 AACAGCAAGAA	181 Prolygalaly
2346 (1-	1.31e-108 Le 1520.00 Ma 100.00% Co 100.00% Mi 100.00% Mi	3/554,GOLN33/569 ndedness: Single; logy: Linear; Location/Qualifiers Location/Qualifiers 1. 1149 /organism="Mastadenovirus" /ord_Lype="genomic DNA" /db_xref="taxon:10509"	INS SECRETARY OF THE DEPAR UN GENOME SCIENCES INC JP 2001523954-A/53 27-NOV-2001 31-MAR-1998 JP 1998541962 HAROLD KLEANTHOUS, LING LI LER, AMAL AL GARAWI AMAL AL GARAWI ANAL AL GARAWI	viruses, no RN 1149) Lissolo,L., To a, and 50 kDa he polynucleotide 11523954-A 53 KN NOV	11 , and 50 kDa polynucleoti :22627956 A/53.	hArgIleGluGluLeu 	hrTyfGluGlnalalybProthrIleLybGlym CTTATGAACAGGCTAAACCTACCATTAAGGGGA	PGGTTATCATATTATC	roabpPheSerLybalaalaPheAlaLeuThrProGlyabpTyrThrLybThr 	AlaGlnAsnGlyGly 	9LysGluAlaLysPho vapaGaaGCTAAATTC
Gaps: 0	h: 1 es: 2 rvative: 0 tches: 0	n/Qualifiers. vvirus" NA."	PARTMENT OF HEAL 962 LISSOLO, JEAN FR	no RNA stage; Adenovirida, Tomb, J.F., Miller, C. a Da helicobacter polypept: btide molecules 53 27-NOV-2001;	49 bp DNA helicobatter pol de molecules.	lArgLysHisAlaLy NAGAAAGCACGCTAA	PLYSGlyMetLeuGl AAGGGGATGTTACA	FYrLeuIleSerLy 	aLeuThrProGlyAs TTAACTCCTGGGGA	/AspLeuGlyLysPh GATTTGGGGAAATT	∃leGluLeuAlaAs ATTGAGTTAGCCAA
	149		O, JEAN FRANCOIS TOMB, CHARLES PA61K31/70, A61K31/715, A61K39/02,	ae. and Garawi,A.A. ldes and	linear PAT 27-AUG-20 polypeptides and	ArgMetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIleValIleAsnLys 299 	rGluGinalaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGlu 280 	LysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyr 260 	aPheAlaLeuThrProGlyABpTyrThrLyBThrProVal 240 	AsnSerLysAsnAlaGinAsnGlyGlyAspLeuGlyLysPheGinLysAsnGinMetAla 220 	rolysalalyslysGluAlalysPheIleGluLeuAlaAsnArgAspThrIleAspPro 200 CAAAGGCTAAAAAGAAGCTAAATTCATTGAGTTAGCCAATCGGGATACGATTGATCCT 705
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Helicobacter pylori 26695
Helicobacter pylori 26695
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1 (bases 1 to 11421)
Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A.,
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Submitted (06-AUG-1997) The Institute for Genomic Submitted 
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FIQTSEGAIKYNGIDMANGMVKTWGERYPHIFVALDHGTTFESGCEKAVKAGFTSDN
ROADHALFERNICATED INTRONKTWGERYPHIFVALDHGTTFESGCEKAVKAGFTSDN
BOFVKESQVDYLAPAIGTSHGAFKFKGEPKLDFERLQEVKRLTNIPLVLAGASAIPDN
BOFVKESQVDYLAPAIGTSHGAFKFKGEPKLDFERLQEVKRLTNIPLVLAGASAIPDN
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TPEFKAMMEAVKKQALVEFWAKKQAEEVKKVQLFEKEMQDFYNAKNQQLFVKQEAHAR
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MAPDFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEK
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/product="fructose-bisphosphate aldolase
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/db_xref="GI:2313265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cell binding factor 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |162. .2085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="HP0176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MKKNILNLALVGALSTSFLMAKPAHNANNATHNTKKTTDSSAGV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Helicobacter pylori 26695"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="HP0175"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity: 45.96; identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ter) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kirkness, E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712
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                                                                                                           /gene="HP0181"
6378. .7052
                                     6378. .7052
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note="hypothetical protein; identified by GeneMark;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mikainishafekplyngvnlhikpkeslailgvsgsgkstlls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MLOPPKIVAELSANHNODLNLAKESLHALKESGADPVKLOTYTE
SCMTLNSKEDPFIGOTLWDKENLYELYQKASTPLEWHAELFELARKLDLGIFSSFS
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RVNNFDITLLKCVSAYPSKIEDANLLSMYKLGEIFGVKFGLSDHTIGSLCPILATTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="spore coat polysaccharide biosynthesis proteing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAIGMSELKKGLKIELGGVPYRIVEYQHVKPGKGAAFVRAKIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L42023 SP:P44626 PID:1003497 PID:1222229 PID:1204555 percent identity: 28.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4843. .6120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLDTTSANQVISMLQNYITEKEGALVLATHDEHLAFTCSQVYRLEKEVLIKEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4205. .4846)
/gene="HP0179"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASMIEKHFILNKSLQTPDSAFSMDFNGFKSMVEAIKQSVLALGEEEPRINPKTLEKRR
FFARSLFVIKDIQKGEALTENNIKALRPNLGLHPKFYKEILGQKASKFLKANTPLSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3179. .4201)
/gene="HP0178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQVPFHVLEGEIIKVNTETEEYLEKVK" complement (3179. .4201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="translation elongation factor EF-P (efp)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HP0180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4843. .6120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HP0180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transT table=11
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to GP:1786703 percent identity: 37.62; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD07248.1"
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/transT_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HP0177"
                                                                                                                                                                                                                                                                                                                                                                                                                         dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to
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REFERENCE AUTHORS	7 AsnLeuAlaLeuValGlyAl	8
	.183A-2 (1-299) x CJCBF2 (1-2006)	US-10-039-:
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	376.50 nilarity: 52.38% Similarity: 33.33% n: 24.77%	Score: Percent Si Best Local Query Matc
CJ11168X2 LOCUS DEFINITION	Scores: 5.57e-20 Length: 2006	ORIGIN Alignment Pred No:
Db 8	NVHGVYKPGNVSLQPEILKNSQKFVKDKFALNSDKPINFVFHGGSGSELKDIKNAVSY GVIKMIDTDTQWAFWDGVREYELKNRAYLQGQIGNPEGDDKPNKKYYDPRVWLRSGE	
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0у 2	/transl table=11	
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0у 2	/gene="fdac"	, de
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Db . 4	D. 73	
07 1	/gene="cbf2" 94915	CDS
Db 3	/db_xref="taxon:197" 94915	gene
0у 1	NA"	
Db 3	se 12006 /organism="Campylobacter jejuni"	Bource
Ογ 1	CHU Poitier, Loca	PEATURES
Db 2	mission (10-FEB-1995) C. Burucoa, Laboratoi	JOURNAL
Q	2 (bases 1 to 2006) Burucoa, C.	AUTHORS
Db 2	96099687 8525063	MEDLINE
γ		JOURNAL
Db 1	Cenatiempo, Y. and Fauchere, J.L. Nucleotide sequence and characterization of peb4A encoding an	TITLE
Q	<pre>Burucoa,C., Fremaux,C., Pei,Z., Tummuru,M., Blaser,M.J.,</pre>	AUTHORS
Db 1		3. Day 2.
Qy	Campylobacter je	SOURCE
DЬ	X84703.1 GI:671839 CBF2 gene; cell binding factor; fdaC gene; fructose 1 6-hishboshbre aldolase	Värsion Käywords

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X 2 5
                                                                                                                                                                                                                                                                                                                                                                                      802 TTTGATGAAGTAAACAAGGTATTGAAAACGGACTTAAATTTGAAGAATTTAAAAAAGTT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742 ACGAATTTTGGTTATCATGTAATCTTAAAAGAAAATTCGCAAGCTAAAGGTCAAATCAAA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 TCAAAAAAC-----CAAGGTGGTGATCTTGGTTTGATCAATCAACTATGGTAAAG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 ATCTTAGTAGCGACAGAAAAAGAACCTAAGGATATTATTAACGAACTTAAAAGGTTTAAAA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 IleLeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnPro 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 GCTTTTTÄTGATCAAÄATÄÄÄÄÄÄAAATATGTAAAACCTGCAAGAGTGCAAGČÄAAAACÄT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862 ATCAATCAAAAAGGCCAAGATCTCTTAAATAGTGCTAAAGTG 903
                                                                                                                                                                                                                                                                                                            282 MetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIle 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 TyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGluArg 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyrThr 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682 CCTTTTACAGATGCTGCTTTCGCGCTTAAAAATGGTACTATTACTACAACTCCGGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 SerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 GGTAAAGAACTAGATGCTAAATTTAGCGAGCTTGCTAAAGAGAAATCAATTGATCCAGGT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 LysAlaLysLysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsn 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 AspPheTyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 TATCAAGAGAAATTTTAAATACTATTAAA-----ATTGATGCGGCTAAAGTTAAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AAAGACCCTTTATACACAAAAGAACTTGATCGTGCAAAAAGATGCAATACTTGTTAATGTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 SerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAlaLeuValGluPhe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AGAGGACAG------GATTTTAAAACTTTGCCAGATAATCAAAAAAAGCTCTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 GTAAATGCAGCTACA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 TrpAlaLysLysGlnAlaGluGluValLysLysValGlnIleProGluLysGluMetGln 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 ACTGTTAATGGCAAGAGCATTAGCGATACAGAAGTAAGTGAATTTTTTTGCCCCCTATGCTT
308601 bp DNA linear BCT 09-JUL-2002 Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6. AL139075 AL111168 AL139075.2 GI:6967817
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Campylobacter jejuni subsp. jejuni NCTC 11168 Campylobacter jejuni subsp. jejuni NCTC 11168 Bacteria; Porteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacter.

Campylobacterales;

Parkhill, J., Wren, B.W., Mungall, K., Ketley, J.M., Churcher, C.,

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of C. jejuni sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Basham,D., Chillingworth,T., Davies,R.M., Feltwell,T., Holroyd,S., Jagels,K., Karlyshev,A., Moule,S., Pallen,M.J., Penn,C.W., Quail,M., Rajandream,M.A., Rutherford,K.M., VanVliet,A., Whitehead,S. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0688204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_jejuni/)
                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Cj0344" unknown, len: 41 aa; no H
/note="Cj0344, unknown, len: 41 aa; no H
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/protein_id="CAB74181.1"
/db_xref="UniProt/TIEMBL:Q9PIF6"
                                                        /EC_number="4.1.3.27"
/note="Cj0345, trpE, possible anthranilate synthase /note="Cj0345, trpE, possible anthranilate synthase component I, len: 416 aa; similar in C-terminal half to component I (EC many e.g. TRPE_CLOTM anthranilate synthase component I (EC 4.1.3.27) (494 aa), fasta scores; opt: 784 z-score: 1209.9 E(): 0, 47.0% identity in 281 aa overlap. 35.6% identity in 365 aa overlap to HP1282. Contains Pfam match to entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Cj0343c, probable integral membrane protein, lengel 161 as, similar to many hypothetical membrane proteins e.g. Y441 METUA MJ0441 (267 as), fasta scores; opt: 152 z-score: 301.8 E(): 1.5e-09, 30.7% identity in 257 as overlap. 45.1% identity to HP0677 and 44.0% identity to
PF00425 chorismate bind, chorismate binding enzyme, 309.50, E-value 3.9e-89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="UniProt/Trembl:Q9PIF7"
/translation="MBITDLPYLIGIISGIASGLEGIGGGMIIVPSMFALGASAHHA
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PILAYFLGYDSKKVVSLSLFEVIFASVSGIISFSNSGVIDSEVIHKGILVGIASMVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Cj0344"
1009. .1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(101. .886)
/gene="Cj0343c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (101. .886)
/gene="Cj0343c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGIKIIEKWHISAHRKILLCVYALSILGTTHSLLNKLNFINF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative integral membrane protein"
/protein_id="CAB74180.1"
/db_xref="GI:6967818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="NCTC 11168"
/db_xref="taxon:192222"
                                                                                                                                                                                                                                                                              gene="trpE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 41 aa; no Hp match"
                                  score
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="anthranilate synthase component II"
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FKRAFHSEIIGSSAYDNAKOLKDILGGRMQGAKFDLVVLNAMFALYTANKASSPLVAK
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YLIYEKNSKMFFKFGASKYFEYLKDDIEPMKKKQKNDFEILNSLEDEKNDFLKMCEKA
KEYLLSGDIFQVVLSKQLCIKHQVNAFDYYESLSALMFSAMFYFPSKYGVVLGSSPE
FILKIKKREIYLAFIAGTRNLENNCDLLALEKDLLSDEKELSEHKMLVDLARNDASKF
GTQTRVENLFSIIKKKFVMHIVSEVYAMKEDASIFDVLEAVFPAGTLSGAFKIRALE
ITSBLEDCDRGIYGGAVGFLMFNEDITLAILIRCAFFTQDKAYLASGAGIVLQSESQK
/note="Cj0347, trpF, probable N-(5'-phosphoribosyl)anthranilate isomerase, similar to many trpF e.g. TRPF_LACCA
                                                                                                                                                                                                                                                                                                     glycosyl transferase
1.1e-37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00117 GATase, Glutamine amidotransferases class-I, score 252.00, E-value 8.4e-72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains PS00442 Glutamine amidotransferases class-I active site and Pfam matches to entry PP00117 GAYase, Glutamine amidotransferases class-I, score 252.00, E-value 8.4e-72 and to entry PF00591 Glycos_transf_3, glycosyl transferase family, score 138.60, E-value 1.1e-37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Cj0346, trpD (trpGD), probable anthranilate synthase component II, len: 53 aa; (contains glutamine amidotransferase and anthranilate phosphoribosyltransferase) similar to many e.g. TRPG_ECOLI anthranilate synthase component II (EC 4.1.3.27) (530 aa), fasta scores; opt: 866 z-score: 781.3 E(): 0, 32.6$ identity in 528 aa overlap. N-terminus has 34.6$ identity to HP1281, C-terminus is 33.2$ identity to HP1280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3143.
                                                                                                                                                                                                                                                                   4134. .4733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMILEAIYSGKVIEYFKEYQAYAKA"
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/note="Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="trpD"
/note="Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry
chorismate binding enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYAEICAKRKALLVAFENLKKENQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="PS00442 Glutamine amidotransferases class-I active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="trpD"
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/EC_number="4.1.3.27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3589
                                                                                                                                                                                                                                                                                                                                   to entry PF00591 Glycos_transf_3, ase family, score 138.60, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00425 chorismate bind, score 309.50, E-value 3.9e-89"
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Query Match:
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                                                                                                                                      GlyValLeuLeuArgGlyThrLy8Ly8GluGluValGluArgGlyMetValLeuCy8Ly8
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Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes
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elongation factor TU; tuf gene.
Wolinella succinogenes
Wolinella succinogenes
Bacteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Wolinella.
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Muenchen, 80290 Muenchem, FRG
Location/Qualifiers
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Direct Submission
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/codon_start=1
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/transT_table=11
/product="elongation factor Tu"
/db_xref="0A:54199.1"
/db_xref="GA:642482"
/db_xref="OA:642482"
/db_xref="UniProt/Swiss-Prot:P42482"
/db_xref="UniProt/Swiss-
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/strain="DSM 1740"
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                                                GluGluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArg
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ThrThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGly
                                    GAGGAAGGCGGACGACACTCCATTCTTCAATGGATACCGACCTCAGTTCTATGTTAGA
                                                                                 AAAATAGGTTCTATCACTCCTCACACTAACTTTGAAGGTGAAGTTTACGTTCTTTCCAAA
                                                                                            LysProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLys
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EF-Tu; transfer RNA-Gly; transfer RNA-Thr; transf tRNA-Gly; transfer RNA-Thr gene; tufB gene; tangylobacter jejuni
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacter.
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Submitted (22-APR-1998) G.
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Conservative:
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2 (bases 1 to 10085)

King, B.L., Alm, R.A. and Trust, T.J.

Direct Submission
Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidney
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A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambrid
MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith,
Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills,
                                                                                                                                                                                                                                                                                 1 (bases 1 to 10085)
Alm, R.A., Ling, L.S., Moir, D.T., King, B.L., Brown, B.D., Doig, P.C., Smith, D.R., Noonan, B., Guild, B.C., deJonge, B.L., Carmel, G., Tummino, P.J., Caruso, A., Uria-Nickelsen, M., Mills, D.M., Ives, C., Gibson, R., Merberg, D., Mills, S.D., Jiang, Q., Taylor, D.E., Vovis, G.F. and Trust, T.J.
                                                                                                                                                                                                                     Genomic-sequence comparison of two unrelated isolates gastric pathogen Helicobacter pylori
Nature 397 (6715), 176-180 (1999)
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Helicobacter pylori J99
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Helicobacteraceae, Helicobacter.
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RES Kleanthous, I., Garawi, A.A., Miller, C., Tomb, J.F. and Oomen, R.P. Identification of polynucleotides encoding novel helicobacter polypeptides in the helicobacter genome Patent: JP 2001527393-A 122 25-DEC-2001;

MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET VACCINS AGROBIOLOGICAL RESOURCES MINISTRY O SA, HUMAN GENOME SCIENCES INC
PN JP 2001527393-A/122
PD 25-DEC-2001
PP 01-APR-1998 JP 1998541947
PR 01-APR-1997 US 08/833457,24-JUN-1997 US 08/881227 PR 29-JUL-1997 US 08/902615
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PI RAYMOND PETER COMEN
PC A01N43/04,A61K31/70
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ThrTyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGlu
                   LysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyr
                                                                         ProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProVal
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Weltzin,R.A. and Guy,B.
LT and CT in parenteral
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Location/Qualifiers
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LeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeu
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                                      TTTTGGGCTAAAAAACAGGCTGAAGAAGTGAAAAAAGTCCCAAATCCCCAGAAAAAGAAATG
                                                                                      PheTrpAlaLysLysGlnAlaGluGluValLysLysValGlnIleProGluLysGluMet
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MAPDFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEK
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/transl_table=11
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Best Local Similarity:
Query Match:
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
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It (bases 1 to 1082)

Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.

Antigenic composition and method of detection for leatent: JP 2001517091-A 50 02-OCT-2001;

GENELABS TECHNOLOGIES INC

PN UP 2001517091-A/50

PD 02-OCT-2001

PD 02-OCT-2001

PD 02-OCT-9001

PD 02-OCT-901

PR 25-APR-1997 US 60/045107, 14-OCT-1997 US

THERESA P CHOW, KIRK E FRY, MOON Y LIM, C P MCATEE PC

C12N15/31, C07K14/205, C07K16/12, A61K39/106

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers.
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                                                                                       AlaLysProAlaHisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSer
  SerAlaGlyValLeuAlaThrValAspGlyArgProIleThrLysSerAspPheAspMet 60
                                                                                                                                                                   ATGAAAAAAATATCTTAAATTTAGCGTTAGTGGGCGCGTTGAGTGCGTCGTTTTTGATG
                                                                                                                                                                                            MetLysLysAsnIleLeuAsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMet
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Helicobacter

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other sequences; artificial sequences.

1 (bases 1 to 1117)

1 (bases 1 to 1117)

1 (chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P. Antigenic composition and method of detection for leatent; JP 2001517091-A 39 02-OCT-2001;

PALENDES TECHNOLOGIES INC
JP 2001517091-A/39

PN JP 2001517091-A/39

PD 02-OCT-2001

PP 25-APR-1997 US 60/045107,14-OCT-1997 US
THERESA P CHOW, KIRK E FRY, MOON Y LIM, C P MCATEE PC
C12N15/31,C07K14/205,C07K16/12,A61K39/106
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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I (bases 1 to 1082)

Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.

Altigenic composition and method of detection for 1
Patent: JP 2001517091-A 303 02-OCT-2001;

GENELABS TECHNOLOGIES INC
PN JP 2001517091-A/303

PD 02-OCT-2001

PN 07 25-APR-1997 US 60/045107, 14-OCT-1997 US
THERESA P CHOW, KIRK E FRY, MOON Y LIM, C P MCATEE PC
C12N15/31, C07K14/205, C07K16/12, A61K39/106

CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Bacteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Helicobacter.
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Sequence 1323 from Patent
AX788859
AX788859.1 GI:32955273
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Patent: WO 02066501-A 1323 29-AUG-2002;
Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Legrain, P., Rain, J.C., Colland, F.,
            GlyValLeuAlaThrValAspGlyArgProIleThrLysSerAspPheAspMetIleLys
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 GGCGTGTTAGCGACAGTGGATGGCAGACCTATCACTAAAAGCGATTTTGACATGATTAAG
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/mol_type="genomic DNA"
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Helicobacter hepaticus ATCC 51449
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.

1 (bases 1 to 303820)
Suerbaum, S., Josenhans, C., Sterzenbach, T., Drescher, B., Brandt, P.,
Bell, M., Droge, M., Fartmann, B., Fischer, H.P., Ge, Z., Horster, A.,
Holland, R., Klein, K., Konig, J., Macko, L., Mendz, G.L., Nyakatura, G.,
Schauer, D.B., Shen, Z., Weber, J., Frosch, M. and Fox, J. G.,
Schauer, D.B., Shen, Z., Weber, J., Frosch, M. and Fox, J. G.,
The complete genome sequence of the carcinogenic bacterium
Helicobacter hepaticus
2 (bases 1 to 303820)
Drescher, B. and Suerbaum, S
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AE017144.1 GI:32
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Submitted (27-MAY-2003) Institute of Hygiene and Microbiology,
University of Wuerzburg, Josef Schneider Str. 2, Wuerzburg D-97080,
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/product="phosphoribosylanthranilate isomerase"
/product="phosphoribosylanthranilate isomerase"
/proteain_id="AP76599.1"
/db_xref="GI:32261549"
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3986. .5032
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                                                                                                                                                                                                                                             lipoprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="trpC"
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/transl_table=11
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                                                                                                                                                                                     GIEIAARVPFIATTLQKADAAGNPKVTASHTYNAGVRYIFSF"
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complement (5633. .6196)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5053. .5607)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7073. .7681)
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                                                                                                                                                                                                                                                                                                                                                                                                               locus_tag="HH0007"
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                                                                                                                                                                                                                                                                                                                                                                                            note="similar to Helicobacter pylori Hop-family proteins"
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C_number="3.1.26.4"
                                                                                                                                          ement (7845.
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                                                                                                                                            .8888)
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US-10-039-183A-2 (1-299) x AE017144 (1-303820)
LysAlaLysLysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsn 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAAAGTATCCCAAACTTCAACTATAATAAGCTTTCTGAGCAAGAAAAAGAAATGCTC
                                                                                                                                                                                                 AAAATTTACCAAGAAAATGAAGGAGAA---TTTATTGACCAAGAAGGTAAAGCACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                    ACTTCTAAAGAATATACTGATACCATTAATAGCATTAAAGGATAATCTCCTTATTGATTTA 104369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÁTTAATGAGCTTÁTÁAATAGGCAACTTATTCTTAAAGCTGCTÁÁÁCAAGÁÁÁAACTAGAT 104309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysGlnArgAsnProAsnPheAspPheAspLysLeuLysGluLysGluLysGluAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaGlyValLeuAlaThrValAspGlyArgProIleThrLysSerAspPheAspMetIle
                                                                                                                                   IleLeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnPro 181
                                                                                                                                                                                                                                                  AspPheTyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAlaLeuValGluPhe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAsp 101
                                                                                     ATTCTTGTAAAATCAGAATCTGAAGCAAAAGAATTATCAAAGAGCTTGATAAAGTAGGT 104546
                                                                                                                                                                                                                                                                                                           TrpAlaLysLysGlnAlaGluGluValLysLysValGlnIleProGluLysGluMetGln 141
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GASGGKGLGIAFLKHIERTGFLLFVLDIMREQSLKEQMEILSLELEKFSPILSQRAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9290. .9604)
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LKALFKRLSFVLLGAILAIFLFAKSTYFELFATKDI
LKALFKRLSFVLLGAILAIFLFAKSTAYGRARWAEKSDIQWGLNCERGFILAFAK
BEWLCVAWALFDELSALYLFTPAKSTAYGRARWAEKSDIQWGLNCERGFILAFAK
KKIKYDTPLSTLVIAPPGTGKTSAIIIPULLSIPNSQVVIDVKGEICSLTAGYRQKKL
LNQVFIFNPGEBSNFHFNPFNLERMSKLGFAEKTAIVRQVGSTIFFKKDEKOSHWR
ETAKTPFEFAAMHNIEKYGYTTLYELTKRFFKKOWTDELEBKYFDEKEKGEELGBEVNF
FRLLLRQIAENETLHDNIRDDARRFLGTPANEFGSVLSTFSTKMSIFGDLRVKELTDQ
NSFMFERLLEBMITLYIKCLEKDIFSLSFIIRILKENSTATVKELKSESTDPKERIYLEL
DEVMRFGELDEMHIELBSISRSYNLPHIFAAGSVAQIRKHYSQEDLEIMLDTWAYGVVE
RANRGQAAEDISKEVGDFTAHKKTTSSQDIKILQSYSTSEEAKRLVTAQDILNIPKDK
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/locus_tag="WS1091"
/note="CONJUGAL TRANSFER PROTEIN TRAG"
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                                                                     VLILATGHKATPILAQANFYFKDRTERQKTKIKKENK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="CONJUGAL TRANSFER PROTEIN (TRAG)"
/protein_id="CAE10185.1"
/db_xref="GI:34483187"
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US-10-039-183A-2 (1-299) x BX571660 (1-349926)
                                                                                                                                AGCGTCTCCTACAGCGAAAAAGCTTCGAGAGAAGGCTCAAGTC 191210
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                                                                                                                                                                                 ArgMetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIle 295
                                                                                                                                                                                                                                  CCCTATGAGGATGTCAAGCCTCAAATCGAGCAGAATCTTAAAAATCCAAAAATTCAGAGAC 191255
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CAGAACTCCAAGGAGTTTAAAGACGCCCTAGAGGATGCGAAAGAGGGTTTGACGCTTGAG
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cbf2 and fdaC genes
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/locus_tag="WS1102"
13628. .16075
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FEQPKWWFYGIIGGIALLYGGTFIVNAIVN"
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Query Match:
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Best Local Similarity:
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                                                                                                                                                               AGAGGACAG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSerSerAlaGlyValLeuAla 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMetAlaLysProAlaHisAsn
ATTCAGCAATATTATGCAAGATTTAATTTTGCAAGATGCTAAAAAACAAAATTTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                         ThrValAspGlyArgProIleThrLysSerAspPheAsp---
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/product="N-(5'-phosphoribosyl)anthranilate isomerase"
/protein_id="Cap4184.1"
/db_xref="G1:6967822"
/db_xref="G0:6967823"
/db_xref="GOA:Q9PIF3"
/db_xref="GOA:Q9PIF3"
/db_xref="Unifrot/Swise-Prot:Q9PIF3"
/db_xref="Unifrot/Swise-Prot:Q9PIF3"
/tassel="Unifrot/Swise-Prot:Q9PIF3"
/tassel="Unifrot/Swise-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry PF00697 PRAI, N-(5'phosphoribosyl)antranilate (PRA) isomerase, 102.30, E-value 9.5e-27"
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/gene="trpB"
/EC_number="4.2.1.20"
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ATCAATCAAAAAGGCCAAGATCTCTTAAATAGTGCTAAAGTG 239942
                                                           MetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIle 295
                                                                                                                            TTTGATGAAGTAAAACAAGGTATTGAAAACGGACTTAAATTTGAAGAATTTAAAAAAAGTT 239900
                                                                                                                                                                                                                                                                                   ThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyrThr 261
                                                                                                                                                                                                                                                                                                                                                                               CCTTTTACAGATGCTGCTTTCGCGCTTAAAAATGGTACTATTACTACAACTCCGGTAAAA 239780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCAAGAGAAAATTTTAAATACTATTAAA-----ATTGATGCGGCTAAAGTTAAA 239486
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Search completed: April 24, Job time: 4774.41 secs 2005, 09:13:30

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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This DNA sequence codes for a 32 kDa Helicobacter pylori polypeptide (see AAW73034) designated GHPO 1360. A polymucleotide encoding the unprocessed, or the mature, GHPO 1360 can be obtained from genomic DNA by PCR amplification (see AAW07969-70 and AAW07973). The invention provides polymucleotides (see AAV72001, AAV07912-21 and AAV07963-64) encoding a
                                                                                                                                                                                New isolated Helicobacter the diagnosis, prevention gastroduodenal diseases.
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                                                                         The invention relates to a method for inducing protective immune response to Helicobacter infection. The method comprising administering to a mammal by injection an immunogenic Helicobacter pylori polypeptide comprising a subunit of H. pylori urease admixed with an adjuvant having one or more heat-liable toxin of Escherichia coli (LT), B subunit of LT (LTB), cholera toxin (CT), and B subunit of CT. The method is useful for inducing an immune response to Helicobacter infection of H.pylori infection. The invention is useful as vaccine. The present sequence is Helicobacter
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                                                      ArgMetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIleValIleAsnLys
                                                                                    ACTTATGAACAGGCTAAACCTACCATTAAGGGGATGTTACAAGAAAAGCTTTTCCAAGAA
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

5.77e-137 1486.00 99.00% 96.99% 97.76%

Length: Matches: Conservative: Mismatches: Indels:

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CC (OMP) having no terminal Phe residue. The protein may be used in a CC vaccine to prevent or treat H. pylori infection or to identify H. pylori CC polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as CC antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific CC antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and CC the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid consequences predicted from various ORF were analysed for significant the other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be consequenced from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
06-DEC-1996;
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P-PSDB; AAW55450.
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                                                                                                                                                                            ACTTATGAGCAAGCTAAACCTACCATTAAGGGGATGTTACAAGAAAAGCTTTTCCAAGAA
                                                                                                                                                                                                                       AMAACAGAGTTTGGTTATCATATTATCTATTTGATTTCTAAAGATAGCCCTGTAACTTAT
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            Y104.1.ASM
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Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
   Helicobacter
pylori.
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05-NOV-1998

25-APR-1998; 98WO-US008487

25-APR-1997; 14-OCT-1997; 97US-0045107P. 97US-0061958P.

(GENE-) GENELABS TECHNOLOGIES

TP, **E** 3 Mcatee ÇP,

1999-009433/01

New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response.

Claim 27; Page 123-124; 402pp; English.

The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunogractivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to center th. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-WAR-2003 to correct PF field.)

Sequence 1082 BP; 383 A; 189 Ç 222 G; 288 Η, 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB: Score: Pred. No.: Scores: 1.78e-136 1482.00 98.33% 97.32% 97.50% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1082 291 5 0

US-10-039-183A-2 (1-299) x AAV90591 (1-1082)

Qy	1 MetLysLysAsnIleLeuAsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMet 20	
뮍	165 ATGANANANATATCTTANATTTTAGCGTTAGTGGGCGCGTTGAGTGCGTCGTTTTTGATG 224	
Q	21 AlaLysProAlaHisAsnAlaAsnAsnAsnAlaThrHisAsnThrLysLysThrThrAspSer 40	
망	225 GCTAAGCCGGCTCATAACGCAGATAACGCTACGCATAACACCAAAAAAAA	
Q	41 SerAlaGlyValLeuAlaThrValAspGlyArgProlleThrLysSerAspPheAspMet 60	
ఠ	285 TCACCCGGCGTGTTAGCGACAGTGGATGGCAGACCTATCACTAAAAAGCGATTTTGATATG 344	
Q	61 IleLysGlnArgAsnProAsnPheAspPheAspLysLeuLysGluLysGluLysGluLysGluAla 80	
망	345 ATTAAGCAAACGAAATCCTAATTTTGACTTTTGACAAGCTTAAAGAAAAAGAAAAAAAGAAGCC 404	
Q	81 LeulleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeu 100	
Вb	405 TTGATTGAGCAAGCTATCCGCACCGCACTTGTAGAAAATGAGGCTAAGGCAGAAAAGCTC 464	
Qy	101 AspSerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAlaLeuValGlu 120	
Дb	465 GATCAGACTCCAGAATTTAAAGCGATGATGGAAGCGGTTAAAAAAACAGGCTTTAGTGGAA 524	

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RESULT 6
AAV90580
ID AAV9
XX AV9
XX AV9
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DT 20-M
DT 18-F
XX Nucl
XX Anti
XX Pept
XX WO98
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                     New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-
                                                          P-PSDB;
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14-OCT-1997;
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                                                                                                                                                                                                                                               Helicobacter
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peptic ulcer;
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18-FEB-1999
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            immune response
                                                                                                                  GENELABS
                                                                                                                                                                                                                                                                   immunogenic cluster family; vaccine; gastritis;
lcer; gastric adenocarcinoma; gastric lymphoma; s
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97US-0061958P.
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Best Local Similarity:
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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunogractivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct pf field.)
Sequence 1117
                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                     Page 119; 402pp; English
     BP; 388 A; 202 C;
     234 G;
     293
     T; 0
       U; 0 Other;
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Match:

1.85e-136 1482.00 98.33% 97.32% 97.50%

Length:
Matches:
Conservative:
Mismatches:
Indels:

1117 291 3 5 0

x AAV90580

(1-1117)

Gaps:

Scores:

5 밁 8 日 S 당 Ś 밁 Ś 밁 5 밁 Ś 밁 δ 맑 Ś 멍 S 밁 á 맑 Ş 843 201 663 603 543 483 423 303 183 221 783 723 181 161 141 121 101 363 243 81 61 41 21 -AlaLysProAlaHisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSer ProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProVal PheTrpAlaLysLysGlnAlaGluGluValLysLysValGlnIleProGluLysGluMet LeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeu ATGAAAAAAATATCTTAAATTTAGCGTTAGTGGGGCGCGTTGAGTGCGTCGTTTTTGATG MetLysLysAsnIleLeuAsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMet HisileLeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGln GlnAspPheTyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArg GATCAGACTCCAGAATTTAAAAGCGATGATGGAAGCGGTTAAAAAAACAGGCTTTAGTGGAA IleLysGlnArgAsnProAsnPheAspPheAspLysLeuLysGluLysGluLysGluLysGluLysGluAla SerAlaGlyValLeuAlaThrValAspGlyArgProIleThrLysSerAspPheAspMet **AACAGCAAGAACGCGCAAAATGGCGGTGATTTGGGGAAATTCCAAAAGAACCAAATGGCT** AsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAla CCAAAGGCTAAAAAAGGAAGCCAAATTCATTGAGTTAGCCAATCGGGATACGATTGATCCT ProLysAlaLysLysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspPro CATATTTTAGTGAAAACCGAAGATGAGGCTAAACGGATTATTTCTGAGATTGACAAACAG TCACCCGGCGTGTTAGCGACAGTGGATGGCAGACCTATCACTAAAAGCGATTTTGATATG TTGATTGAGCAAGCTATCCGCACCGCACTTGTAGAAAATGAGGCTAAGGCAGAAAAGCTC 160 240 200 722 180 662 602 140 542 120 100 80 362 60 302 40 242 20 902 842 220 782 482 422

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US-10-039-183A-2 (1-299) x AAV90844 (1-1082)
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                                                                          No.:
                                                                                                        Sequence 1082
                                                                                                                                                                                                                                                            Claim 20;
                                                                                                                                                                                                                                                                                         New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-
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14-OCT-1997;
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18-FEB-1999
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                                                                                                                                                                                                     CCGGATTTTNCTAAAGCCGCTTTCGCTTTAACTYCTGGGGATTACACTAAAACCCCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 844
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          The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to detect H. pylori-specific antibodies, for diagnosing infection or to detect meaning the protect against H.
                                                                                                                                                                     New Helicobacter pylori antigens and related nucleic aciuseful in serological diagnosis and protective vaccines, lasting immune response.
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P-PSDB; AAW89814.
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peptic ulcer;
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                      Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                           H. pylori ORF 03xe11215orf7.
                                                                                                                              AAV24638;
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This sequence encodes a Helicobacter pylori protein of unspecified CC function. The protein may be used in a vaccine to prevent or treat H. CC pylori infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors. The CC DNA and probes derived from it may be used for the identification of H. CC pylori in a sample, and the diagnosis of H. pylori infection. Nucleic CC acid sequences complementary to the DNA act as antisense sequences, and CC can be used to prevent the translation of H. pylori mRNA. Antibodies CC against the protein can be used in immunoassays to evaluate the abundance and interest protein (ATCC 55679) was determined from overlapping contigs generated CC by mechanically shearing the bacterial DNA. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated CC defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF CC were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR camplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5,6; Page 155; 1145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-503122/46.
P-PSDB; AAW55229.
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Sequence 456 BP; 170 A; 79 Ç 106 G; 101 7, 0 U; 0 Other;

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                                           US-10-039-183A-2 (1-299) x AAV24638
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           MetLysLysAsnIleLeuAsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMet
 ATGAAAAATATATCTTAAATTTAGCGTTAGTGGGCGCGTTGAGCGCGTCGTTTTTGATG
                                                                         7.91e-58
679.00
96.60%
92.52%
44.67%
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                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                Gaps:
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AlaLysProAlaHisAsnAlaAsnAbnAlaThrHisAsnThrLysLysThrThrAspSer 40

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                                                   The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence encodes a selected interacting domain (SID), identified via
                      Sequence 595
                                           protein-protein interactions
                                                                                                                                             Claim 7;
                                                                                                                                                                    ulcers in mammals.
                                                                                                                                                                            New complexes of protein-protein interactions in Helicobauseful for identifying modulating compounds for treating
                                                                                                                                                                                                                 P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Protein-protein interaction; gene; ds.
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P-PSDB; AAR21691.
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22-JUL-1992
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  Nucleotide andaminoacid sequence of protein-B-pertussis -
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(first entry)
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Best Local S Query Match:

Pred. No.:

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US-10-039-183A-2 (1-299) x AAQ22604 (1-960)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 960 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           improve the immune response. (Updated on 25-MAR-2003 to correct PI
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aAlaPheAlaLeuThrProGlyAspTyrThrLysThrProValLysThrGluPheGlyTy
                                                      CGCGGCGGCGACCTGGGT----TGGGCGCTGCACCAACTACGTCCAGCCGTTTGCCGAGGC
                                                                                         AsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaPro-AspPheSerLysAl
                                                                                                                                                                       ---AAGTTCGACGATCTGGCCAAGAAGAACTCCAAGGACCCCGGCAGCCC-----GAG
                                                                                                                                                                                                               AlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGln
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                                                                                                                                                                                                                  Alignment
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ADS02896

standard;

DNA;

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Percent Similarity:
Best Local Similarity:
Query Match:

1.31e-12 224.00 42.77% 25.60% 14.74%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

993 85 57 100 90

US-10-039-183A-2 (1-299) x ADS02896

(1-993)

Pred. No.: Alignment S

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cc sequence with any of 3772 fully defined nucleate deguences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as CC given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); CC producing an S. epidermidis polypeptide, an isolated mucleic acid CC comprising a nucleotide sequence of at least 8 nucleotides in length; a cyaccine composition for prevention or treatment of an S. epidermidis polypeptide above and a carrier; treating cc infection, composition for prevention or treatment of an S. epidermidis cc infection; detecting the presence of a Staphylococcus mucleic acid in a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis cc infection; detecting the presence of a Staphylococcus mucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based computer based system for identifying fragments of the Staphylococcus genome of the Staphylococcus plasmids of commercial importance; a computer based system for identifying fragments of the Staphylococcus genome of the staphylococcus g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 200
P-PSDB;
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13-AUG-1998;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing a treating an S. epidermidis bacterial infection.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated nucleic acid comprising a nucleotide
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                                                                                                                                                                                 GlyMetLeuGlnGluLysLeuPheGlnGluArgMetAsnGlnArg-----
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                                                                               GATGCATACAAAGAATTATTAAAAGAGTATAAAGTA 870
                                                                                                                                                   TCAAATATCAAACAAÄÄÄTTÄATCGAAGÄÄAAGGTACAGAAGAAACCTAAATTATTAACT
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               DNA;
                 1720
                 ВP
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                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antilisteria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; SEQ ID NO 3354; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-332479/37.
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29-AUG-2002
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AlaGlyValLeuAlaThrValAspGlyArgProIleThrLysSerAsp----PheAspMet 60
                                                                                                                                                                   LysProAlaHisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSerSer 41
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                              IleLysGlnArgAsn------ProAsnPheAspPheAspLysLeu-----
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ABQ70541/ ID ABQ7

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1171 GATAAATACAAAGTAAGCGACGAAGATGTTGATAAGAAATTC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 ThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnProLysAlaLysLys 185
  595
                                                   284
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                                                                                                265 AlaLysProThrIleLys---GlyMetLeuGlnGluLysLeuPheGlnGluArgMetAsn 283
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AAAACGCTTAAAAAAGAATACAAAGATGCTAACGTAAAAGTG 554
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GCAGCTTAIGCCCTTAAAAACAAAGGCGACATCAGCGCTCCAGTAAAAACACAATACGGA 707
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                                                GlnArgIleGluGluLeuArgLysHisAlaLysIleValIle 297
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US-09-252-991A-13635

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23, Appl
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138, Appl
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1193, Ap
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3178, Ap	Sequence	21-976-	4	497	8.3	•	43	
32	Sequence	-09-596-002-3	4	62909	8.4	127	42	G
6011,	Seguence	-09-489-039F	4	1764	8.4	128	41	
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371	Sequence	-09-328-352-371		1881	8.6	131	38	
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1, Appli	Seguence	-09	4	32998	9.4	142.5	35	O
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	Sequence	US-09-408-020-67	4	279	9.4	142.5	33	
	Sequence	US-09-252-991A-3440	4	1218	9.5	144	32	
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12902, A	Seguence	US-09-252-991A-12902	4.	1113	9.9	٠	26	
851	Sequence	-252-991A-85	4.	1344	10.0	•	25	
818	Sequence	-252-991A-81	4.	1296	10.0	•	24	O
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386	Sequence	US-09-252-991A-3865		1224	11.2	171	20	
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3694,	Sequence	-09-252-991A-36		1869	11.4	174	18	a
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ALIGNMENTS

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LENGTH: 1149
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Patent No. 6576244
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guy, Bruno
TITLE OF INVENTION: IT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US/09/100,258
PRIOR FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weltzin, APPLICANT: Guy, Bro
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                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (106)...(1002)
                                                                                                                                                            FEATURE:
NAME/KEY: Big_peptide
LOCATION: (106)...(166)
                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Helicobacter pylori
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Sequence 8077, Application US/0990;
Patent No. 6833447;
GENERAL INFORMATION:
APPLICANT: GOldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: States, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xe
FILE REFERENCE: 38-10(15849)B
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; ORGANISM: Myxococcus
US-09-902-540-8077
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                                                                    SASnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaProAspPh
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              CGACGAAGTGGTATTCAAGCTGGGGGGTGGGGCAGGTTTCGGACGTG--
                                                                                                                                                                                              GTACGGCGCGCACGAGAAGGACTTCCACGAGCCCGAGCAGGTCCACGCCGCGCAAATCGT
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US-09-902-540-824/c
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LENGTH: 7811
TYPE: DNA
ORGANISM: MYXOCOCCUB XBNThUB
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 05/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR SEQ ID NOS: 16825
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 BLY8GlnAlaGluGluVal---LY8LY8ValGlnIleProGluLY8GluMetGlnA8pPh 143
                                       GGGGGTGCTGCGGCTGTCCGGGGACTATCCGGCGGCAACTTCAACGAGGTCCTGGCCCA 2193
                                                                                                                                                                                             GÉTÉCTECTECAGGAGGÉGEGCAAGCACAACGTCACCGTCACCCGGAGGAGGAGGTGGACCG 2253
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US-09-134-001C-974
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 974
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APPLICANT: Lynn Dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Sequence 13635, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13635
LENGTH: 2097
TYPE: DNA
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                                            TyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyrThrTyrGluGlnAla 265
                                                                                 GCGCTGTATGCGCTGAAGCAAGGTGAG---GTATCCGCCCCGGTGAAGACTCCGTACGGC
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Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13809
LENGTH: 2331
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FAPELICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity:
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                                        GCCAACCTCTCCGAGCAGCGCGATGCCGCCCACATCCTGATCGAGGTGAACGACAAGGTC 1444
                                                                                                                         GACCAGGTCAAGGTGAAGCAGGAAGACCTCGAGGCGTTGTAC-----CAGAAGGAAATC 1504
                                                                                                                                                             LysLysValGlnIleProGluLysGluMetGlnAspPheTyrAsnAlaAsnLysAspGln 150
                                                                                                                                                                                                        TTCATGACTCCCGAGCAGGTGGTCGAATACGTGGAACTGAAGAAGTCCTCCTTCTTC 1558
                                                                                                                                                                                                                                                                                         TCCAAGAGCAGCGTGAGCGAGGACGAGGTGAAGGCCTTCTACGAAGGCCCACAAGAGCGAG 1618
                                                                                                                                                                                                                                                                                                                                                                        TTCGCTCGCCTCGAGAAGCAGACCCGCGACTTCGCCACCCTGGCGATCAAGGCCGACGCT 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAG---CTTCGCGCCGGCCTGGCGGGCACCGGTTTCGTCACCGACAACGAATTGCAGTCC 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAlaIleArgThrAlaLeu-------ValGluAsnGlu------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValAspGlyArgProlleThrLysSerAspPheAsp---MetIleLysGlnArgAsnPro
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                                                                                                                                                                                                                                                                                                                                                                                                               ---AlaLysThrGluLysLeuAsp------
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                                                                            LeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLysThrGluAsp-----
-----GluAlaLysArgIleIleSerGluIleAspLysGlnProLysAlaLysLys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TACAGCCGCATGCAGTTCCGCCAGATGCTCGGCCAGGAAATGCTCATCGGC 1795
                                                                                                                                                                                                                                               ----LysGlnAlaLeuValGluPheTrpAlaLysLysGlnAlaGluGluVal
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211.50
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Matches:
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OTHER INFORMATION: Incyte template ID No. 6632636;
PUBLICATION INFORMATION:
US-09-596-002-33
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                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                            Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 33
LENGTH: 63563
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Patent No. 6632636
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CURRENT FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/140,121 PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Patterson, Chandra APPLICANT: Berg, Kim, L. TITLE OF INVENTION: NUCLEOTIDE
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: M. catarrhalis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSerThrProGlu-----
                                                                                                                           GGCAGACCT----TCATCTGATGCTCAATTTATCAAGCAAGCATTAGATAAAGAAATT 11808
                                                                                                                                                             GlyArgProIleThrLysSerAspPheAspMetIleLysGlnArg-----AsnProAsn
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                                                      TTTGACAGCACCAATCTAATCGCCTCAAGCCAACCTTTACCAAATATCACTGTAAAT 11868
                                                                                        PheAspPheAspLysLeuLysGluLysGluLysGluAlaLeuIleAspGlnAlaIleArg
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US-08-956-171E-168
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GENERAL INFORMATION:
                                                                                                                                                Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
Commerce: Maryland
Commerce: Maryland
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ZIP: 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12571
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGATATTATT 12582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGATCGATCGGCTTAATCAA-----AGCCACAATCGAGATAGTGATTTATTGAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08956171E
                                                                                                                                                                                                                                                                                                                                                                                                                 Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GlnIleProGluLγs---GluMetGlnAspPhe 143
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SEQUENCE CHARACTERISTICS:
LENGTH: 7963 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                         4681
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                   4630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 LysGluAlaLeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThr 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSerSerAlaGlyVal 44
                                                                                            AsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLysThr 166
                                                                                                                                                                                                                                                                                                                                                   AGCAATACGGCGGTAAAGATAAATTTGAA------AAGGCCCTTCAACAGCAAGGT 4680
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                                                                                                                                                                                                                                                                                                                                                                                         GluLysLeuAspSerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAla 117
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FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/791,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                           TTAACA------GCCGATAAATATAAAGAAAATTTACGTACTGCTGCTTATCATAAA 473
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TELEFAX: (301) 309-8439
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43.30%
26.17%
13.59%
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                                                                       -GACAGCARGAAAĠĊTTCAĊAĊĂTŤŤÄATTÁÄAGTT 4815
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RESULT 9
US-08-781-986A-168
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 US-08-781-986A-168
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Patent No. 6737248
GENERAL INFORMATION:
                                                                   TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7963 base pairs
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                           NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PBS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATTACTATCAGATAAAATTAAAATCTCTGATTCTGATATTAAAGAA------
LysLeuPheGlnGluArgMetAsnGlnArgIleGluGluLeuArg-LysHisAlaLysIl
                                                                                                                                                                   ThrLysThrProValLysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAsp 255
                                                                                                                                                                                                                                        LyaAanGlnMetAlaProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAapTyr 235
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                                                                                             SerProValThrTyrThrTyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGlu
                                                                                                                                   TCAGAGGTT---GTTAAATCAAGCTTTGGATATCATATT
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                                                                                                                                                                                                                                                                                                                        AspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGln 215
                                                                                                                                                                                                                                                                                                                                                                  GAAATTCAAAAAGAA----GTTTCAAAAGATCCAAGTAAATTTGGTGAAATCGCTAAAAAA
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Mismatches:
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PACENT NO. 6673910
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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LENGTH: 1110
TYPE: DNA
ORGANISM: M.catarrhalis
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                AlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGly
                                                                TTGATCGATCGGCTTAATCAA-----AGCCACAATCGAGATAGTGATTTTATTGAGTTT
                                                                                    TyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeu
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SEQ ID NO 3927
LENGTH: 1371
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANTION: Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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ORGANISM: Myxococcus xanthus
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                AACCAGGCGAAGGTCGTCTTCGCGCGCCTTCCTGCCGGCCATGTACGCCGACAAGGTCCCC
                                               LysGlnAlaLeuValGluPhe-----
                                                                                                            AlaLysThrGluLysLeuAspSerThrProGluPheLysAlaMetMetGluAlaValLys 114
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RESULT 12
US-09-902-540-1193/c
US-09-902-540-1193, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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                                                                                                                                     Alignment Scores:
                                                                                                                                                                                US-09-902-540-1193
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1193
LENGTH: 21375
TYPE: DNA
ORGANISM: Myxococcus xanthus
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                FEATURE:

NAME/KNY: unsure
LOCATION: (1)..(21375)

OTHER INFORMATION: unsure at all n locations
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           US-09-57-884-1
(Sequence 1, Application US/09557884)
; Sequence 1, Application US/09557884
; Patent No. 6506581
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: The Nucleotide sequence of the Haemophilus influenzae of the Haemophilus in
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  SEQUENCES:
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Best Local Similarity:
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1067915
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APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
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                                                             GAAGTTTTCTTCAAAAGCGTTTAGCTCGTTTAGCAACTTTATCTCTTGCAGATGAAATG
                                                                                                                             AATGGC-----GTTGCTAACAGTGAATTTATTGTTCCTGCTCAAGTAAAAAAATAGCGCA 1067854
                                                                                                                                                          AspGlyArgProIleThrLysSerAspPhe-----AspMetIleLysGlnArgAsn
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COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                            IleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSerThrProGlu 105
                                                                                             ProAsnPheAspPheAspLysLeuLysGluLysGluLysGluAlaLeuIleAspGlnAla 85
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STRANDEDNESS: double
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RESULT 14
US-09-643-990A-1
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                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATB: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1068452 TTAGAAAAACAAGCGAGTGATAAGGCTTTTGAAGACAGCAAGTCTCTTAATA
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ADDRESSEE: Human Genome Scientification of the STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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COUNTRY: U
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APPLICATION NUMBER: 08/487,429 FILING DATE: 1995-06-07
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Owen White
Hamilton O. Smith
J. Craig Venter
OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
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US-09-643-990A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067561 CTTCGTCAAAACATCGTTAATCTAATGATCAAGAATTACTTCGCCAATATGTTAAA 1067620
                                  1068128 GCAAATGAACAAGATGCGAAAGTGGCTTACGAGGAATTA------CAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067681 TTTCAAGTAAAGGGTAAATTTGATÄÄTÄČTGTTTATCAACGAATATTACAACAAAAATCAT 1067740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1067621 GAATTAAAATTAGGCGTGAGTGATGAAATGATTAAAACGTGCAATCGTGACCGATCCTAAT 1067680
                                                                                                                                                                     1068017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
   185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                     GCAAAACAATCAGTCTCTGATGAAATCAAAACGTATTATGAAGCTAATCAAAAGTCT
                                                                                                                                                                                                                                                                                                                            IleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSerThrProGlu
                                                                                                                                                                                                                                                                                                                                                                         GAAGTTTTCTTTCAAAAGCGTTTAGCTCGTTTAGCAACTTTATCTCTTGCAGATGAAATG 1067914
                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGGC-----GTTGCTAACAGTGAATTTATTGTTCCTGCTCAAGTAAAAAATAGCGCA 1067854
 LysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsn 204
                                                                                                   CAAGATAATAAAGCACAA---TTTATGACTCAA-----CATTTAGCTCATATTCAATTT 1068127
                                                                                                                             AsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuVal
                                                                                                                                                                    TCTGCAGATAACATCAGTAGAAATCTTCAAGTTACAGATGTAGAAATTGCGCAATATTAT
                                                                                                                                                                                                 GlnAlaGluGluVal---LysLysValGlnIleProGluLysGluMetGlnAspPheTyr 144
                                                                                                                                                                                                                                    TTT---GTTCAGCCAGAGCAGGTTAAAGTTCAG------TATATTGATCTT 1068016
                                                                                                                                                                                                                                                                  PheLysAlaMetMetGluAlaValLysLysGlnAlaLeuValGluPheTrpAlaLysLys 125
                                                                                                                                                                                                                                                                                                                                                                                                        ProAsnPheAspPheAspLysLeuLysGluLysGluLysGluAlaLeuIleAspGlnAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspGlyArgProIleThrLysSerAspPhe-----AspMetIleLysGlnArgAsn
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                                                                LysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnProLysAlaLys
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Matches:
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US-10-039-183A-2 (1-299) x US-09-252-991A-3818 (1-825)
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Best Local Similarity:
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US-09-252-991A-3818
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LENGTH: 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1068452 TTAGAAAAACAAGCGAGTGATAAGGCTTTTGAAGACAGCAAGTCTCTTAATA 1068503
146 AlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuVal---
                                                                                                                                                                                                                                                                                                                                      100 LeuAspSer------ThrProGluPheLysAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGluArg-Met----
                                                                                                                                                                                                                                            109 MetMetGluAlaValLysLysGlnAlaLeuValGluPheTrpAlaLysLysGlnAlaGlu 128
                                                                                                                                                                                                                                                                                                    193 GCCGACGCGCTGGGCATCGAGGCCCGCTGCGAAGACGGCGAGACGCCGGAG------
                                                                                                                                                                                             -----GAAGCGCGCATCCGCCAATTGCTGGAGGAA------
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                                                                                                                                                                                                                                                                                                                                                                                                           GCGCTGGCGCTGGAGGCCGCCTGCCGTGCGCTGATCGTCCGCCAGTTGCTCCTGCAACGG
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                                                                                                                                        GluValLysLysValGlnIleProGluLysGlu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLys 99
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                                                                                      GAGGTGCAGGTCCCGGAAGCCGACGAAGACGCCTGCCGGACCTGGTACGCG
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Search Job t	DЬ	Ş	Db	Ş	Db	ફ	DЪ	Ş	망	ঠ	망	Ş	망	Ş	Вb	ঠ	Ъ
Search completed: April 24, 2005, 11:43:22 Job time : 1174.78 secs	Db 778 ATC 780	Qy 295 Ile 295	Db 718 GTGCAGGTGTTGCAGCGAGCGGTGGGACAGTACATCGGCGTGCTGGGGAGACGCCTGT 777	275	Db 658 GAAGGCGGCGAGCCGCGCTCGACTTCGACGCGCGCACAGATCGCCGCGCACCTGCAG 717	255	598	235	Db 541 GAGCCGGGGCAGACCGTCCCCGAATTCGAGAAGCGCCTGCTGCGCCGCGCGCG	215	490	Qy 195 ArgAspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPhe 214	Db 445 GACGAGTTGCGCGGGCATCCCGAGCGCTTCGTCGACCTGGCCCGG 489	175	Db 385 TGCGCGCCGGACGACCTGGAAGGCCGCGAGACGGCGCGAAGCAGGCCGCGGAGCTGCTC 444	165	Db 325 GCCAATCCGGGGCGCTTGCTCGGCCCCTGGCGAATTGCGCCCATGTGCTGCTGGCC 384
			TGT 777	Lyв 294	3CAG 717	1Gln 274	3CGC 657	:Гув 254	3 597	Asp 234	ATC 540	Phe 214	CGG 489	Asn 194	CTC 444	lle 174	3GCC 384

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-Qg/Qgn2 I/USPTO spool/USI0039183/runat 22042005 122426 20167/app query.fasta_1.1038
-DB-Published Applications NA -QFMT=fastap -SUFFIX-rnpb-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST=45 -DOCALIGN=200 -THR SCORE-pct - THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=20000000 -USER-US10039183 @CGN 13 894 @runat 22042005 122426 20167
-NCFU=6 -LOCPU=3 -NO MAXB -LARGEQUERY -NEG SCORE-SC -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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Copyright (c) 1993 - 2005 Compug
                                                                                                                      /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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(f)ptodata/1/pubpna/PCT_NEW_PUB.seq:*
(6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
(6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
   6/ptodata/1/pubpna/US60
6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

US-09-881-752A-243

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Sequence 243, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleanthous; Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in 171TLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
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SEQ ID

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; LOCATION: (51)...
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                                                   LysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyr
                                                                                                  ProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProVal
                                                                                                                                                                                                                                       CATATTTTAGTGAAAACCGAAGATGAGGCTAAACGGATTATTTCTGAGATTGACAAACAG
                                                                                                                                                                                                                                                      HisIleLeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGln
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ThrTyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGlu
                                                                                       CCGGATTTTTCTAAAGCCGCTTTCGCTTTAACTCCTGGGGATTACACTAAAACCCCTGTT
                                                                                                                                        AACAGCAAGAACGCGCAAAATGGCGGTGATTTGGGGGAAATTCCAAAAAGAACCAAATGGCT
                                                                                                                                                      AsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAla
                                                                                                                                                                                       CCAAAGGCTAAAAAAGAAGCTAAATTCATTGAGTTAGCCAATCGGGATACGATTGATCCT
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US-08-831-310-1
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Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and C
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/03700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
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OTHER INFORMATION:
NAME/KEY: Signal Sequence LOCATION: 106...166
OTHER INFORMATION:
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TELEX:
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                  AlaLysProAlaHisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSer
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 CGCATGAATCAACGCATTGAGGAACTAAGAAAGCACGCTAAAATTGTTATCAACAAG 947
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APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Polypeptides and Corresponding Pol
TITLE OF INVENTION: Polypeptides and Corresponding Pol
FILE REFERENCE: 06132/037002
CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 08/831,310
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1149
                                                                                                                                                                                                                                                       RESULT 3
US-10-039-183A-1
; Sequence 1, Application US/10039183A
; Publication No. US20030143242A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: CDS
LOCATION: (106)...(1002)
FEATURE:
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    ThrTyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGlu
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...900;
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-335-977-483
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                                                                                US-10-039-183A-2 (1-299)
                                                                                                                                              Percent Similarity:
Best Local Similarity:
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US-10-335-977-483
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                                                                                                                               Query Match:
                                                                                                                                                                              Score:
                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)42-4214
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               .
No.:
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                             FEATURE:
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STATE: Massachusetts
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                                                                                                                                           Sequence 482, Application US/10335977

Sequence 482, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR
                                                                                                              NUMBER OF SEQUENCES: 10031
                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProVal
                                                                                                                                                                                                                                                                                             CGCATGAATCAACGCATTGAGGAATTAAGGAAGCACGCTAAAATTGTTATCAACAAG
                                                                                                                                                                                                                                                                                                              ArgMetAsnGlnArgIleGluGluLeuArgLysHisAlaLysIleValIleAsnLys 299
                                                                                                                                                                                                                                                                                                                                                                                                                                            LysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProLysAlaLysLysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisIleLeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnAspPheTyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGGGCTAAAAAACAGGCTGAAGAAGTGAAAAAGATCCCAAATCCCCAGAAAAAAAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspSerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAlaLeuValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLysProAlaHisAsnAlaAsnAsnAlaThrHisAsnThrLysLysThrThrAspSer 40
                                                                                                                                                                                                                                                                                                                                                            ACTTATGAGCAAGCTAAACCTACCATTAAGGGGATGTTACAAGAAAAGCTTTTCCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                ThrTyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                            AAAACAGAGTTTGGTTATCATATTATCTATTTGATTTCTAAAGATAGCCCTGTAACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPAGGCTAPAPAGAGCCAPATTCATTGAGTTAGCCAPTCGGGATACGATTCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCAGACTCCAGAATTTAAAGCGATGATGGAAGCGGTTAAAAAAACAGGCTTTAGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleLysGlnArgAsnProAsnPheAspPheAspLysGluLysGluLysGluLysGluLysGluLysGluLi
                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGCAAGAACGCGCAAAATGGCGGTGATTTGGGGGAAATTCCAAAAGAACCAAATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATATTTTAGTGAAAACCGAAGATGAAGCCAAAAGGATTATTTCTGAGATTGACAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheTrpAlaLysLysGlnAlaGluGluValLysLysValGlnIleProGluLysGluMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGATTGAGCAAGCTATCCGCACCGCGCTTGTAGAAAATGAGGCTAAGGCAGAAAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGCAGGCGTGTTAGCGACAGTGGATGGCAGACCCATCACCAAAAGCGATTTTGATATG
                                                                                ADDRESSEE:
                                                               28 State Street
                                                                                LAHIVE & COCKFIELD
                                                                                                                               DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                               897
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CURRENT APPLICATION DATA:

Sin

COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

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Percent Similarity:
Best Local Similarity:
Query Match:
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LOCATION: (B) LOCATION 1...504
SEQUENCE DESCRIPTION: SEQ ID NO: 482:
US-10-335-977-482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-039-183A-2 (1-299) x US-10-335-977-482 (1-504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
PILING DATE: 17-DEC-1997
ATTORNEY AGENT INFORMATION:
NAME: MANDATE: AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)242-4214
INFORMATION FOR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                               301
                                                                                                                                                           211
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 361
                               251
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                                                                                                                                                                                                                                                                                                                                                                                                       131 LysLysValGlnIleProGluLysGluMetGlnAspPheTyrAsnAlaAsnLysAspGln
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                  LeuIleSerLy8A8pSerProValThrTyrThrTyrGluGlnAlaLy8ProThr---Ile 269
                                                                                                                                                 LeuGlyLysPheGlnLysAsnGlnMetAlaProAspPheSerLysAlaAlaPheAlaLeu
                                                                                                                                                                                                             GluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAsp
                                                                                                                                                                                                                                                                             LysArgIleIleSerGluIleAspLysGlnProLysAlaLysLysGluAlaLysPheIle
                                                                                                                                                                                                                                                                                                                                           LeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLysThrGluAspGluAla 170
                                                                                  ThrProGlyAspTyrThrLysThrProValLysThrGluPheGlyTyrHisIleIleTyr 250
                                                                                                                                                                                                                                                                                                                         CTTTTTGTCAAGCAAGAAGCCCATGCTAGGCATATTTTAGTGAAAACCGAAGATGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                     AAAAAGATCCAAATCCCAGAAAAAGAAATGCAGGATTTTTACAACGCCAATAAAGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/335,977 FILING DATE: 30-Dec-2002 R APPLICATION DATA:
TIGATITICTAAAGATAGCCCTGTAACTTATACTTATGAGCAAGCTAAACCTACAGAGTTA
                                                                                                                                                                                           GAGTTAGCCAATCGGGATACGATTGATCCTAACAGCAAGAACGCGCAAAATGGCGGTGAT
                                                                                                                                                                                                                                                         TTGGGGAAATTCCAAAAGAACCAAATGGCTCCGGATTTTTCTAAAGCCGCTTTCGCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.04e-62
745.50
91.76%
87.06%
49.05%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33128
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NAME/KBY: misc feature
LOCATION: (B) LOCATION 1...456
SEQUENCE DESCRIPTION: SEQ ID NO: 481
US-10-335-977-481
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                          US-10-039-183A-2 (1-299) x US-10-335-977-481 (1-456)
                                                                                                                                                                                                                                   Alignment Scores:
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US-10-335-977-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANDITURE, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)727-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 481:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 481, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
RELATING TO HELICOBACTER PYLORI FOR
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 ArgLysHisAlaLysIleValIleAsnLys 299
16 ATGAAAAATATATCTTAAATTTAGCGTTAGTGGGCGCGTTGAGCGCGTCGTTTTTGATG
                      MetLysLysAsnIleLeuAsnLeuAlaLeuValGlyAlaLeuSerThrSerPheLeuMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTAGCACGCTAAGTGTTATCAACAATAGA 504
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                   2.37e-56
679.00
96.60%
92.52%
44.67%
                                                                                                                                                                                                                                                                                                                                                                           pylori
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
  75
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1079

1019

92

73

60

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RESULT 7
US-10-398-221-3354/c
; Sequence 3354, Applic
; Publication No. US200
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome an
FILE REFERENCE: 344 702 - US /10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 3354
LENGTH: 1720
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Query Match:
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Best Local Similarity:
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                                                                                                                              US-10-039-183A-2 (1-299) x US-10-398-221-3354 (1-1720)
                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                   US-10-398-221-3354
                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(end)
OTHER INFORMATION: n can
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Listeria monocytogenes
FEATURE:
                                                                1354
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Publication No. US20040018514A1
GENERAL INFORMATION:
            TITLE OF INVENTION: Listeria innocua, geno FILE REFERENCE: 344 702 - US CURRENT APPLICATION UMBER: US/10/398,221 CURRENT FILING DATE: 2003-03-27 PRIOR APPLICATION UMBER: PCT/FR 01/03 061 PRIOR FILING DATE: 2001-10-04 PRIOR APPLICATION NUMBER: FR 00/12 697 PRIOR FILING DATE: 2000-10-04
                                                                                                                                              APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
NUMBER
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LENGTH: 43980
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LOCATION: (1)..(end)
OTHER'INFORMATION: n can be
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GCAGCTTATGCCCCTTAAAAACAAAGGCGACATCAGCGCTCCAGTAAAAACTCAATATGGA
                  AlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProValLysThrGluPheGly 245
                                                         GAAAACGGTGGCCAATTAGCACCATTTGGTTCTGGTAAAATGGATCCTGCATTTGAAAAA
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                                                                                                                                             GluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAla
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US-10-398-221-2058
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US-10-398-221-2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Listeria innocua, genome and applications FILE REFERENCE: 344 702 - US CURRENT APPLICATION NUMBER: US/10/398,221 CURRENT FILLING DATE: 2003-03-27 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 PRIOR FILING DATE: 2001-10-04 PRIOR PPLICATION NUMBER: FR 00/12 697 PRIOR APPLICATION NUMBER: FR 00/12 697 PRIOR FILING DATE: 2000-10-04 NUMBER OF SEQ ID NOS: 4025
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TYPE: DNA
2353051 GCTCAÑAGTGGCTTÑACTGÁGAAATCATTCAAAAGCCÑÁCTTAAGTACAACTTATTAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAATTAATTCTTGGACTTGTCATGATGGCATTG-----TTCAGTCTAGCA
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                                          LysGlnAla---LeuValGluPheTrpAlaLysLysGlnAlaGluGluValLysLysVal 133
                                                                                                                                         GTACAACAACTTACTTTCGAAAAAATCCTTGGTGATAAATACAAAGTAAGCGATGAAGAT 2352990
                                                                                                                                                                                                                                      IleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAsp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaGlyValLeuAlaThrValAspGlyArgProIleThrLysSerAspPheAspMetIle
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                                                                                          GTTGATAAAAAATTCAAAGAGTACAAATCCCAATACGGCGATCAATTCTCTGCAGTTTTA 2353050
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APPLICANT: LAGACE, Robert, E.
APPLICANT: PATTERSON, Chandra
APPLICANT: BERG, Kim, L.
APPLICANT: BERG, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MOR
FILE REFERENCE: ELITRA.025C1
CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 63563
TYPE: DNA
ORGANISM: Moraxella catarrhalis
US-10-672-787-33
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US-10-672-787-33
; Sequence 33, Applicat:
; Publication No. US200;
; GENERAL INFORMATION:
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PheAspPheAspLysLeuLysGluLysGluAlaLeuIleAspGlnAlaIleArg
                                      GGCAGACCT----TCATCTGATGCTCAATTTATCAAGCAAGCATTAGATAAAGAAATT 11808
                                                                        GlyArgProlleThrLysSerAspPheAspMet[]eLysGlnArg-----AsnProAsn
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No. US20040067554A1
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US-08-781-986A-168
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                                                                                                                                                                                                                              Sequence 168, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: HP Vectra 486/33
                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                STREET: 9410 Key
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                        ADDRESSEE:
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TITGACAGCACCAATCTAATCGCCTCAAGCCACCAAACTTTACCAAATATCACTGTAAAT 11868
                                                                                                                                                                                                                                                                                                                                                                                                           AlaLysIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAAGCAGGAGGGTAGGCAGCTGAGCTTTGAAGAGGCATATCCTATCATTGAAAAATCAT 12510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLysAspSerProValThrTyrThrTyrGluGlnAlaLysProThrIleLysGlyMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGGTATCAGTATTAATĆĆĠATTGAAÁĆÁCGATATĞĞĠATCĆÁŤGTGÁŤTGAAGTTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGATCGATCGGCTTAATCAA-----AGCCACAATCGAGATAGTGATTTTATTGAGTTT 12282
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;;;|||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGTGATTGAGTGCTTGGGCGAGAGGGCGTGGCTAGAGAATGAAGAAGCTACCATCGCT 12048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCATGCTAATCAAGTTGAATTTGTTAGTATGCCAATAATGACGCTTCGCCATATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----MetMetGluAlaValLysLysGln 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSerThrProGlu-----
                                                                                                                                28: Human Genome Scien
9410 Key West Avenue
                                                                                                                                                      Genome Sciences,
                                                                                                                                                                                              Staphylococcus aureus Polynucleotides and Sequences 5255
                                                                                                                                                                                                                                                                                                                                                                                                             296
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                  .50 inch,
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                      1.4Mb
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OPERATING SYSTEM:

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-781-986A-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 150
SEQUENCE CHARACTERISTICS:
LENGTH: 7963 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BENSON, BOD

REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24f
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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    4816 AAATCTAAGAAAAGCGACMAAGAAGGCTTAGATGATAAAGAAGCGAAACAAAAAGCTGAA 4875
                                                                                                                                                                                                                                                                                                                               4630
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                                          167
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                                                                                                                                                                GAATTACTATCAGATAAAATTAAAATCTCTGATTCTGAAATTAAAGAA-------
                                                                                                                                                                                                                                                                                    LeuValGluPheTrpAlaLysLysGlnAlaGluGluValLys---------
                                                                                                                                                                                                                                                                                                                                                                   GluLysLeuAspSerThrProGluPheLysAlaMetMetGluAlaValLysLysGlnAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGluAlaLeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGCATCATTTACTGAAATGTTAAATAAAATTTTAGCTGATAAATATAAAAATAAAGTT 4590
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                                                                                                                      AsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLysThr 166
                                                                                                                                                                                                                                                TTAACA-----GCCGATAAATATAAAGAAAATTTACGTACTGCTGCTTATCATAAA
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                                                                                                                                                                                                    -LysValGlnileProGluLysGluMetGlnAspPheTyrAsnAla 146
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Indels:
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Conservative:
                                      -GluAspGluAlaLysArgIleIleSer 175
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TELEFAX: (301) 309-
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS
                                                  PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

AFFERENCE/DOCKET NUMBER: PB248P11

TELEPHONE: (230) 314-1224

TELEPHONE: (230) 314-1224
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MEDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/329,624 FILING DATE: 27-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295
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5. US20040043037A1
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Patrick S. Dillon
                                          309-8439
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID US-10-329-624-168
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   TCAGAGGTT---GTTÄÄÄTCAAGCTTTGGÄTÄTCÄTÄTT-----ÄTTÄÄÄAGCTGÄT
                             ThrLysThrProValLysThrGluPheGlyTyrHisIleIleTyrLeuIleSerLysAsp
                                                                      AAAGGACAAACTGATAAAGATTTTGAAAAAGCACTATTTAAGCTTAAAGATGGTGAAGTA
                                                                                                       LysAsnGlnMetAlaProAspPheSerLysAlaAlaPheAlaLeuThrProGlyAspTyr 235
                                                                                                                                            GAATCAATGGATACTGGTTCA-----GCTAAAAAAAGATGGCGAATTAGGTTATGTTCTT
                                                                                                                                                                                                                   GAAATTCAAAAAGAA---GTTTCAAAAGATCCAAGTAAATTTGGTGAAATCGCTAAAAAA
                                                                                                                                                                                                                                              GluIleAspLysGlnProLysAlaLysLysGluAlaLysPheIleGluLeuAlaAsnArg 195
                                                                                                                                                                                                                                                                                     AAATCTAAGAAAAGCGACMAAGAAGGCTTAGATGATAAAGAAGCGAAACAAAAAGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuValGluPheTrpAlaLysLysGlnAlaGluGluValLys---------
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US-10-470-048B-173

; Sequence 173, Application US/10470048B

; Publication No. US20050037444A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 173
LENGTH: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MEINKE ET AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Staphylococcus aureus
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370 GAATTACTATCAGATAAAATTAAAATCTCTGATTCTGAAATTAAAGAA--
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                                                                                                                                          AGCAATACGGCGGTAAAGATAAATTTGAA-----AAGGCCCTTCAACAGCAAGGT 318
                                                                                                                                                                                                                                                LysGluAlaLeuIleAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThr
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                                                                                                       LeuValGluPheTrpAlaLysLysGlnAlaGluGluValLys-----
                                                                                                                                                                                                                   AATGATAAGAAGATTGACGAACAAATT-----
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205.50
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                             -LysValGlnIleProGluLysGluMetGlnAspPheTyrAsnAla 146
                                                                      GCCGATAAATATAAAGAAAATTTACGTACTGCTGCTTATCATAAA
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369

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417

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168 64

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.0

SEQ ID NO 1250

LENGTH: 1163

TYPE: DNA

ORGANISM: Listeria monocytogenes-4B

US-10-398-221-1250
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US-10-398-221-1250/c
                                                                                  US-10-039-183A-2 (1-299) x US-10-398-221-1250
                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                         Alignment Scores
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                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and
FILE REFERENCE: 344 702 - US
1024 GACAAAACACTTAAAAAATACTATGAAACATGGCAACCAGATATTACTGTAAGC-----
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                                      GluLysGluMetGlnAspPheTyrAsnAlaAsnLysAspGlnLeuPheValLysGlnGlu 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GACAGCAAGAAAGCTTCACACATTTTAATTAAAGTT
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                                                                                                                  1.08e-09
200.50
51.53%
33.13%
13.19%
                                                                                                                    Mismatches:
Indels:
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                                                                                (1-1163)
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Publication No. US20040018514A1

GENERAL INFORMATION:

APPLICANT: GLASER, Philippe

TITLE OF INVENTION: Listeria innocua, genome

FILE REFERENCE: 344 702 - US

CURRENT APPLICATION NUMBER: US/10/398,221

CURRENT FILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

PRIOR APPLICATION NUMBER: PC 00/12 697

PRIOR PILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 4025
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Best Local Similarity:
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                                                                             US-10-039-183A-2 (1-299) x US-10-398-221-8 (1-495269)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n can be any nucleotide: a,
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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    273998 TTAAAAAAAGTGATTTCCCTA-------GTAGCAGCGACACTACTTTTACTC 274045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluLysLeuPheGlnGluArgMetAsnGlnArgIleGluGluLeuArgLysHisAlaLys
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                                                                              274778 GCAGCTAATATCGATATT 274795
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                                                                                                                                                                                                                                                                                                                                                                                                                                     213 LysPheGlnLysAsnGlnMetAlaProAspPheSerLysAlaAlaPheAlaLeuThrPro 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ValGlnIleProGluLysGluMetGlnAspPheTyrAsnAlaAsnLysAspGlnLeuPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 ValLysLysGlnAlaLeuValGluPheTrpAlaLysLysGlnAlaGluGluValLysLys 132
                                                                                                               292 HisAlaLysIleValIle 297
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                                                                                                                                                                                                                                                                                                                                          GlyAspTyrThrLysThrProValLysThrGluPheGlyTyrHisIleIleTyrLeuIle 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTAAAGAGTACTCAACAGAT-----ACTGCAACTAGCACAAATGGCGGACTATTAGAT 274543
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                                                                                                                                                                                                MetLeuGlnGluLysLeuPheGlnGluArgMetAsnGlnArgIleGluGluLeuArgLys 291
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-MODEL-frame+ p2.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US10039183/runat_22042005_122425_20124/app_query.fasta_1.1038
-Q-/cgn2_1/USPTO_spool/US10039183/runat_22042005_122425_20124/app_query.fasta_1.1038
-DB=EST -QFMT=fastap -SUFFIX=rst -NINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blt -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039183_GCGN_1 1_5533_grunat_22042005_122425_20124 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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      229
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AQ242234
CL982381
AG266881
CL982316
BZ549176
CF842872
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ALIGNMENTS

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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BH369380/c LOCUS . COMMENT DEFINITION JOURNAL MEDLINE PUBMED TITLE ORGANISM Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftu Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardner, M.J. and Collins, F.H.

Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the malaria mosquito Anopheles gambiae

Mol. Genet. Genomics 268 (6), 720-728 (2003) Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftuseigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. BH369380 701 bp DNA AG-ND-155G10.TF ND-TAM Anopheles gambiae AG-ND-155G10, genomic survey sequence. BH369380 BH369380.1 GSS. Other_GSSs: AG-ND-155G10.TR 12655398 (bases 1 to 701) GI:17315481 linear GS: genomic clone Loftus, B.J., GSS 10-DEC-2001 African

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Query Match:
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Best Local Similarity:
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Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnProLys 182
GCCCAATTCCAGGAATCGCTGCGCGAAAAGGCCCAAGATC
                        AsnGlnArgIleGluGluLeuArgLysHisAlaLysIle
                                                                            GAGGAAGTCAAGCCCCAGATCGTGCAGCAGCTGCAA---
                                                                                                                 GluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGluArgMet
                                                                                                                                                         CAGTTCGGCTACCACATCATCCGCCTGGACGATTCACGCCAGGCCGAGCTGCCCAAGTTC
                                                                                                                                                                                            GlupheGlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyrThrTyr
                                                                                                                                                                                                                                                                           PheSerLysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProValLysThr
                                                                                                                                                                                                                                                                                                                      ----GGCGCCCGTGGCGGTGACCTCGACTGGGCCAACCCCGGCAACTACGTGCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="AG-ND-155G10"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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ACCESSION
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AUTHORS
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ242234 705 bp
4P12-64f Ochrobactrum anthropi
genomic clone 4P12-64f, genomic
AQ242234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288
Fax: 864 656 4293
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100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 705)
Tomkins, J., Miller-Smith, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales, Brucellaceae; Ochrobactrum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Class: BAC ends
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AsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaProAspPheSerLysAla
                                                                     GCCAAGTTCGAGGACCTCGCCAAGGAGAGCTCAACCGAC-----GGCACGGCAGCC
                                                                                                              AlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGln
                                                                                                                                                                                                                                                                                                                                                                                                                      //addition, 624 randomly chosen BAC Library"
//clone lib="Ochrobactrum anthropi BAC Library"
//note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Ochrobactrum anthropi Is an important microbe
having potential for the bioremediation of environments
contaminated by aliphatic compounds. We have constructed
a BAC library for O. anthropi that provides a 90x genome
coverage based on an estimated genome size of 3.83 Mb.
The library contains 3072 clones with an average insert
size of 112 kbp. High-density colony filters of the
library were made and a physical map of the genome
constructed using a hybridization without replacement
strategy. In addition, 624 randomly chosen BAC clones
were HindIII fingerprinted and anylized using fingerprint
Contig (FPC; Sangre Centre, UK). The FPC results closely
supported and verified the hybridization contig data.
After deterimining a reduced tiling path of 69 clones,
138 BAC ends were sequenced for a genome wide survey of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                             gene distribution and gene structure.
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/mol_type="genomic DNA"
/db_xref="taxon:529"
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217.50
61.47%
42.20%
14.31%
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Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Be
Tel: 86-10-80481559
 852
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 2256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome
An analysis of transcriptional regulation of the rice genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CL982381 2256 bp DNA linear GSS 21-SEP OBIFSCO47527 Oryza sativa Express Library Oryza sativa (indica
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice genomic sequence.
Class: exon-trapped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 86~10-80488676
Email: chenchen@genomics.
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                               LysAlaMetMetGluAlaValLysLysGlnAlaLeuVal-Glu---PheTrpAlaLysLy
                                                                  CGCCGTGCCATGGCTCAA----CGCGCTGAAGCCGCAGGATTGGAGAAGGACCCGGAAGTC
                                                                                   ArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSerThrProGluPhe
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
                                                                                                                                                                                                                                                                                                                    /clone_lib="Oryza sativa
/note="Oryza sativa exon
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AG266881
                                                                                                                                                                                           2 (bases 1 to 669)
Goto, T., Todo, K., Miyamoto, K. and Akimoto, S.
Direct Submission
Submitted (23-UUN-2003) Takatsugu Goto, Wakayama Medical
University, Department of Microbiology; Kimiidera 811-1,
Wakayama 641-0012, Japan (B-mail:t-goto@wakayama-med.ac.:
Tel:81-73-441-0640, Fax:81-73-448-1026)
                                                                                                                                                                                                                                                                                                                                Goto, T., Todo, K., Miyamoto, K. and Akimoto, S.
Bacterial artificial chromosome library of Finegoldia
29328 for genetic mapping and comparative genomics
Microbiol. Immunol. 47 (12), 1005-1016 (2003)
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Bacteria; Firmicutes; Clostridia; Clostridiales;
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                                                                                                                                                                               ocation/Qualifiers
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  Ma,L., Wa
Jiao,Y.,
                                                                           GSS.

Oryza Bativa (indica cultivar-group)
Oryza Bativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                             CL982316 2850 bp DNA linear GSS OBIFSCO47288 Oryza sativa Express Library Oryza sativa (cultivar-group) genomic, genomic survey sequence.
CL982316 CL982316.1 GI:52419116
                                                              Ehrhartoideae;
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                               nartoideae; Oryzeae; Oryza. (bases 1 to 2850)
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Wangc,J., Chen,C., Liu,X., Su,N., L., Sun,N., Zhang,X., Bao,J., Sun,D.,
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Beijing Institute of Genomics
Chinese Academy of Sciences, I
Tel: 86-10-80481.55
Fax: 86-10-80488676
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An analysis of transcriptional reg
its comparison to Arabidopsis
Unpublished (2004)
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IleTyrLeuIleSerLysAspSerProValThrTyrThrTyrGluGlnAlaLysProThr
                                     LeuThr---ProGlyAspTyrThrLysThrProValLysThrGluPheGlyTyrHisIle
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/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates
Psedomonas acruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ549176 DNA linear GSS 17-DEC. pacs1-60_1717.s1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_1717, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington Box 352145, Seattle, WA Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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eTrpAlaLysLysGln-----AlaGluGluValLysLysValGlnIleProGluLysGl
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                                               rThrProGluPheLysAlaMetMetGlu---AlaValLysLysGlnAlaLeuValGluPh
                                                                                                           -----CTTACGGAAAGGCCCACCAAGGAGCCGAAGTTCCATTG
                                                                                                                                        eAspGlnAlaIleArgThrAlaLeuValGluAsnGluAlaLysThrGluLysLeuAspSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pseudomonas/
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="pacs1-60_1717"
/clone_lib="pacs1-60"
note="clinical isolate 1-60 Whole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 Dp mRNA linear EST 30-OCT-200 psHB022xK01f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB022K01 5, mRNA sequence.

CFB42877
                                                                                                                                                                                       FORWARD: BK reverse primer BACKWARD: BK reverse primer Plate: 022 row: K column:
                                                                                                                                                                                                                                   1880 Pratt Dr., Blacksburg,
Tel: 540-231-7318
Email: bmtyler@vt.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora sojae
Phytophthora sojae
                                                                                                                                                     Plate: 022 row: K column: 01
Seq primer: BK reverse primer
High quality sequence stop: 543
                                                                                                                                                                                                                                                                                                                                             Tyler, B. Not Published 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                               Tyler, B.
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/tissue_type="mycellum"
/cell_line="p6497"
/dev_stage="48 hr. post_infection
/lab_host="Soybean_plant"
                                                            /organism="Phytophthora
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sHB022K01"
                                                                                                                             1. .543
                                                                                                                                        ocation/Qualifiers
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MY-17-E-09 PinfestansMY Phytophthora infestans
BE776559 BE776559.1 GI:10230214
EST.
                                                                                                                  Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau
                                                                                                                                                                                                                                 (bases 1 to 666)

Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.

Initial assessment of gene diversity for the oomycete pathog

Phytophthora infestans based on expressed sequences

Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                         Binnenhaven 9, P.O.Box 8025, 6700
                                                                                                                                                                       Wageningen University
                                                                                                                                                                                                  Contact: Govers F
                                                                                                                                                                                                                                                                                                                   Eukaryota; stramenopiles; Oomycetes;
                                                                                                                                                                                                                                                                                                                               Phytophthora infestans (potato late blight agent)
Phytophthora infestans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspTyrThrLysThrProValLysThrGluPheGlyTyrHisIleIleTyrLeuIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheGlnLysAsnGlnMetAlaProAspPheSerLysAlaAlaPheAlaLeuThrProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnArgAspThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGAAGGAGCTG-----CAGGCGGCCGACGACCTTGGAGGCCACGTTCGCGGCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGGTCGCGGCCAGATGGTGCCCGAGTTCGACAAGGTGGCGTTCGAGAAGCCCCGTGGGG
/db_xref="taxon:4787"
/dev stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
                                                               /organism="Phytophthora
/mol_type="mRNA"
                                                                                                      Location/Qualifiers
                                                   strain="DDR7602, A1 mating type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.69e-10
177.50
55.45%
41.58%
                                                              type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GTCAAGACGCAGTTTGGATGGCACTTGGTGCTGATCACGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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Indels:
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                                                                              infestans"
                                                                                                                                                         EE,
                                                                                                                                                                                                                                                                                                                   Pythiales;
                                                                                                                                                         Wageningen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543
42
38
3
                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                   Pythiaceae;
                                                                                                                                                           The
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                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                 pathogen
                                                                                                                                                            Netherlands
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AUTHORS
TITLE
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BE776294
LOCUS
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ORGANISM
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Best Local Similarity:
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DB:
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MEDLINE
PUBMED
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/clone lib="PinfestansMY"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of p. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."

Scores:

9.33e-09 Length: 666
169.50 Conservative: 14
Sinilarity: 42.39% Miamatches: 32
h: Indels: 7
Gaps: 3
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US-10-039-183A-2 (1-299) x BE776559
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                                                                                                                                                                           Laboratory of Phytopathology Wageningen University Binnenhaven 9, P.O.Box 8025, Tel: 31 317 483 138 Fax: 31 317 483 412
                                                                                                                                                                                                                                                                                                        I (bases 1 to 629)

I (bases 1 to 629)

Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the comycete pathog
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Phytophthora infestans (potato late blight agent)
Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE776294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE776294
MY-14-A-10 PinfestansMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
                                                                                                                                                                                                                                                                       Contact: Govers
                                                                                                                                                                                                                                                                                         10587472
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; stramenopiles;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrIleAspProAsnSerLysAsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGAGATGGTACCGCAGTTTGACAAGGTGGTGTTTGAAGGAGAAGTGGGCGAGCTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Francine.Govers@medew.fyto.wau
                             /organism="Phytophthora infestans'
|mol_type="mRNA"
|mol_type="mRNA"
|strain="DDR7602, A1 mating type"
|db_xref="reaxon:4787"
|dev_stage="4-week old vegetative.
             / {
m dev} stage="4-week old vegetative, non-sporulating mycelium in synthetic medium"
                                                                                                                                          Location/Qualifiers
lab_host="E.
                                                                                                                         .629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:10229949
coli, strain
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Phytophthora
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E
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a infestans cDNA,
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                                                                                                                                                                                                                  Wageningen,
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Best I

Alignment

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/ Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                         Binnenhaven 9, P.O.Box 8025, 6700 EE,
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          BE776554 672 bp mF MY-17-E-04 PinfestansMY Phytophthora BE776554
                                                                                                                                                                                                                 1 (bases 1 to 672)
Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                       Laboratory of Phytopathology Wageningen University
                                                                                                                                                                       Contact: Govers F
                                                                                                                                                                                                                                                                                                              Eukaryota; stramenopiles; Oomycetes;
                                                                                                                                                                                                                                                                                                                            Phytophthora infestans (potato late blight agent) Phytophthora infestans
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                                                                                                                                                                                                                                                                                                                                                                           BE776554.1 GI:10230209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AAGGGCGGTGACTTGGGTACGTTCGACCACGCGCCAGATGGTGCCTGAATTCGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaProAspPheSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLys 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCATCTCGTG---CTGATCTCCCGT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrHisIleIleTyrLeuIleSerLys 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGAGGCTGAGGCCGACGACCTGAGTGTGCAGCTGGGAGAA-----GCCTCCAACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="PinfestansMY"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; Total
RNA was isolated from mycelium of p. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
/organism="Phytophthora
/mol_type="mRNA"
/strain="DDR7602, Al mat
                                                1. .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.03e-08
161.00
56.88%
39.45%
10.59%
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                                infestans
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                                                                                                                       Wageningen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
19
39
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                                                                                                                        The
                                                                                                                                                                                                                                                                                                                                                                                                                       EST 20-SEP-2000
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AG613321/c
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REFERENCE
AUTHORS
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REFERENCE AUTHORS

TITLE

COMMENT

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KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION VERSION

RESULT 10 BE776554

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 ThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnProLysAlaLysLys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                 2 (bases 1 to 658)
Hayashi,K., Morooka,N. and Horiuchi,T.
Direct Submission
Submitted (19-JAN-2004) Takashi Horiuchi, National Institute for
Submitted (19-JAN-2004) Takashi Horiuchi, National Institute for
Basic Biology, Gene Expression and Regulation II; 38 Nishigo-naka,
Myodaijicho, Okazaki, Aichi 444-8585, Japan
(E-mail:kishori@nibb.ac.jp, Tel:81-564-55-7690, Fax:81-564-55-7695)
                                                                                                                                                                                      A more accurate sequence comparison coli K12 W3110 and MG1655 strains
                                                                                                                                                                                                                                                                                                                    Escherichia coli K12
Escherichia coli K12
                                                                                                                                                                                                                                                                                                                                                             AG613321.1
GSS.
                                                                                                                                                                                                                                  Hayashi, K., Morooka, N., Mori, H. and Horiuchi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                        Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG613321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AAGGGCGTGACTTGGGTACGTTCGACCGCGGCCAGATGCTGCCTGAATTCGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCATCTCGTG---CTGATCTCCCGT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrHisIleIleTyrLeuIleSerLys 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAsnLysAspGlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLys 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaProAspPheSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="PinfestansMY"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev stage="4-week old vegetative, non-sporulating mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/clone_lib="PinfestansMY"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4787"
/dev_stage="4-week ol
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K12 MG1655 I
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match: DB:

150

Percent Similarity:

Local Similarity:

1.26e-07 159.50 51.11% 35.56% 10.49%

Alignment Scores:

No::

ORIGIN

USA and

end

pacificus

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US-10-039-183A-2 (1-299) x AG613321 (1-658)
               Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                              CL680822 774 bp DNA PRI012b_H01_2 - PRI012b_BR (774) Mixed pacificus var. California Pristionchus
                                                                                           AppaDB: an AcedB database for the nem Pristionchus pacificus Nucleic Acids Res. 32 (1), D421-D422 Contact: Sommer RJ
                                                                                                                                                                                        Neodiplogasteridae; Pristionchus.
1 (bases 1 to 774)
                                                                                                                                                                                                                             Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
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/db_xref="taxon:83333"
/clone="454-4F"
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/mol_type="genomic DNA"
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="This sequence is an updated part of the sequence
from AE000111-AE000510 series. The first three characters
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for the nematode satellite
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               JOURNAL
                                                         TITLE
                                                                                             AUTHORS
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hasti Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates Psedomonas aeruginosa library J. Bacteriol. (2002) In press Contact: Chris K. Raymond
                                                                                                                                                                                                             GSS.
                                                                                                                                                                                                                                                 pacs2-164 7593. y2 pacs2-164 Pseudomonas aeruginosa pacs2-164 7593, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This library was generated at C sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends.
                                                                                                                                                                        Pseudomonas aeruginosa
Pseudomonas aeruginosa
                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                 BZ568565.1 GI:27201734
                                                                                                                                                                                                                                                                                                          BZ568565
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                                                                                                                                                                                                                                                                                                                                                                                  TyrGluGlnAlaLysProThrIleLysGlyMetLeuGlnGluLys
:::|||:::||||||||||||
-----TAATAGCAAGGCCTTCTCCAGGAGAAG
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                                                                                                              (bases 1 to 972)
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/mol type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P.
var. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector:
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48
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184 219 164

336

205 393 185 435 165 495

JOURNAL COMMENT

Evolutionary Biology

00497071601498

REFERENCE AUTHORS

Srinivasan,J.,

Otto, G.W.,

Pseudomonadales;

Hastings, M.

489 276

261

462

420

372

224

318 204 261

genomic clone GSS 17-DEC-2002

TITLE

ACCESSION VERSION

CL680822 CL680822.1 GI:50187782

survey sequence.

KEYWORDS

SOURCE ORGANISM

Pristionchus pacificus

RESULT 12 CL680822 LOCUS

DEFINITION

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262 234 242 282 225

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Percent Similarity:
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University of Washington
Box 352145, Seattle, WA 98
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washingt
Class: shotgun
                                                                                                                                                                             LysAlaAlaPheAlaLeuThrProGlyAspTyrThrLysThrProValLysThrGluPhe
                                                                                                                                                                                                                                                                                                                        GTCGGCGACGAGCAGGCCAAGGCGAAGATCGACGAGATC-----AAGGCTCGCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValLysLysGlnAlaLeuValGluPheTrpAlaLysLysGlnAla------GluGlu 129
GCTACCAAGGACTTGGAAAGCTCCGCC
                       ArgIleGluLeuArgLysHisAla 293
                                                                             AlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGluArgMetAsnGln
                                                                                                       GGCTACCACCTGATCAAGCTGCTGGGGCGTGCAGGCGCCGGAAGTACCGAGCCTGGAAAGC
                                                                                                                               GlyTyrHisIleIleTyrLeuIleSerLysAspSerProValThrTyrThrTyrGluGln
                                                                                                                                                             GAGGCGCTGTATGCGCTGAAGCAAGGTGAG----GTATCCGCCCCGGTGAAGACTCCGTAC
                                                                                                                                                                                                               GCCGCCACCGGCGTGACCTGGGCTACGCCGGTCGCGGCGTGTACGACCCCGCGTTCGAG
                                                                                                                                                                                                                                    AlaGlnAenGlyGlyAepLeuGlyLyePheGlnLyeAsnGlnMetAlaProAspPheSer
                                                                                                                                                                                                                                                                    AAGGGCGAGGATTTCGCCGCGCTGGCCAAGGAGTTCTCCCAGGATATCGGCTCG-----
                                                                                                                                                                                                                                                                                              LysGluAlaLysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsn
                                                                                                                                                                                                                                                                                                                                        -----GluAlaLygArgIleIleSerGluIleAspLysGlnProLygAlaLys
                                                                                                                                                                                                                                                                                                                                                                             CAAACCINTICCGAACAAGCGCGATTGCCGCCCAACATCCTGATCGAGGTGAACGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                       GlnLeuPheValLysGlnGluAlaHisAlaArgHisIleLeuValLysThrGluAsp---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTTGAAAGAATGTCCTTCCTTTNTTTGGAACCGGGTCCAGGGTTAAAGGCAAGAAAAG
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                                                     CTCAAGCCGAAGCTCGAGGACGAACTGAAGAAACAGATGGTCGAGCAGCGCTTCGTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="pacs2-164_7593"
/clone_lib="pacs2-164"
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Matches:
Conservative:
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BZ574276
LOCUS
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Best Local Similarity:
Query Match:
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University of Washington
Seattle, WA
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genomic survey sequence.
BZ574276
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Tel: 2062216954
Fax: 2066857244
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Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole-Genome-Sequence variation Psedomonas aeruginosa library
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Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: shotgun.
                                                                                                                                                        GCGGAGACCGAGAAGCTGGCGCAGAAGCTGTACGAGCGCATCCAGTCCGGGGAAGAC---
                                                                                                                                                                                                                                                                                                                   AspGluAlaLysArgIleIleSerGluIleAspLysGlnProLysAlaLysLysGluAla
                                                                                                                                                                                                                                                                                                                                                    GTCCGTGACGAAGTGCATGTCCGCCATATCCTGCTCAAGCCCAGCGAAATCCGCAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                 ValLysGlmGluAlaHisAlaArgHisIleLeuValLys-----ThrGlu
AlaLysProThrIleLysGlyMetLeuGlnGluLysLeuPheGlnGluArgMetAsnGln
                                                                                             AACGATACCCCGCAGGCGAGCTGTCCAAG---CCGTTCCGCTCGCAGTTCGGCTGGCAC
                                                                                                                                                                                                                         ---TTCGGCGAACTGGCGAAGAGCTTCTCCGAAGATCCGGGTTCC----GCCCTCAAC
                                                                                                                                                                                                                                                      LysPheIleGluLeuAlaAsnArgAspThrIleAspProAsnSerLysAsnAlaGlnAsn
                               ATCCTGCAGGTCCTCGGCCGTCGCGCCACCGACAGCAGCAGCAGAAGTTCCGCGAGCAGCAG
                                                             IleIleTyrLeuIleSerLys-----AspSerProValThrTyrThrTyrGluGln
                                                                                                                       PheAlaLeuThrProGlyAspTyrThrLysThrProValLysThrGluPheGlyTyrHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pseudomonas
/mol_type="genomic DNA"
/strain="MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:287"
/clone="msh2_3590"
/clone_lb="msh"
/clone_lb="msh"
note="Environmental isolate. Whole genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library."
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Conservative:
Mismatches:
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ACCESSION
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                           ORIGIN
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 386
                       204 AsnAlaGlnAsnGlyGlyAspLeuGlyLysPheGlnLysAsnGlnMetAlaProAspPhe 223
                                                              446
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                                                                                                                                           164 ValLysThrGluAspGluAlaLysArgIleIleSerGluIleAspLysGlnProLysAla 183
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VBI
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502 bp mRNA linear BST 30-OCT-2003 psHB025xG18f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB025G18 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 025 row: G column: 18
Seq primer: BK reverse primer
High quality sequence stop: 502.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF843490
CF843490.1 GI:38059144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1880 Pratt Dr., Blacksburg, VA 24061, Tel: 540-231-7318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyler, B. Not Published Unpublished (2003) Contact: Tyler B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phytophthora.
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                                                              ----AAGGGAGGGACCTGGGGTCCTTCGGTCGCGGCCAGATGGTGCCCGAGTTC
                                                                                                                              TGGCTGCGCCAGATCCGCGACGAGGCCTACGTGGAAATCAAGCAG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgIleGluGluLeuArgLysHisAlaLysIleValIleAsnLys 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 502)
                                                                                                                                                                                                                                                                                                                                                                /organism="Phytophthora sojae"
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db xref="taxon:67593"
/dlone="sHB025G18"
/tissue_type="mycelium"
/tissue_type="mycelium"
/cell_line="p6497"
/dev_stage="48 hr. post infection stage"
/lab_host="8oybean plant"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_sHB"
/note="Vector: pBK-CMV; Site_1: BccR1; Site_2: Xho1"
                                                                                                                                                                                                                                7.16e-07
151.50
54.95%
39.56%
9.97%
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                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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336
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Regult
No.
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-MODEL=frame+_p2n.model -DEV=xlh
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_Bpool/US10039183/runat_22042005_122424_20098/app_query.fasta_1.1038
-Q=/Cgn2_1/USPTO_Bpool/US10039183/runat_22042005_122424_20098/app_query.fasta_1.1038
-DB=N_Geneseq_16Dec04_-QPMT=fastap_-SUFFIX=rng_-MINMATCH=0.1_-LOOPCL=0
-UNITS-bits_-START=1_END=-1_-MATRIX=blosum62_-TRANS=human40.cdi
-LOOPEXT=0_-UNITS-bits_-START=1_END=-1_-MATRIX=blosum62_-TRANS=human40.cdi
-LIGT=45_-DOCALICN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-MAXIEN=2000000000
-LOOPEXT=0_-DOCALICN=200_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXIEN=2000000000
-USER-US10039183_0CGN_1_1_796_0runat_22042005_122424_20098_-NCUG=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-MAIT_-DSPELOCK=100_-LONGLOG_-DSPELOCHEY_-NEG_SCORES=0_-MAIT_-DSPELOCK=100_-LONGLOG_-DSPELOCHEY_-NEG_SCORES=0_-MAIT_-DSPELOCK=100_-LONGLOG_-DSPELOCHEY_-NEG_SCORES=0_-MAIT_-DSPELOCK=100_-LONGLOG_-DSPELOCHEY_-NEG_SCORES=0_-MAIT_-DSPELOCK=100_-LONGLOG_-DSPELOCHEY_-NEG_SCORES=0_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, CC their use in the discovery of novel antibiotics, the essential genes CC themselves and the encoded proteins. The prokaryotes used are Escherichia CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, CC pseudomonas aeruginosa aureus, Salmonella typhi, Klebsiella pneumoniae, CC useful for the identification of potential new targets for antibiotic CC development. The antisense nucleic acids can also be used to identify CC proteins used in proliferation, to express these proteins, and to obtain CC antibodies capable of binding to the expressed proteins, and to obtain CC antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The can used to screen compounds in rational drug discovery programmes. The contisense nucleic acids sequence is also useful to screen for homologous CC useful are proliferation protein. Note: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic formation protectly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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P-PSDB; AAU35822.
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Yamamoto RT,
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Xu HH;
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US-10-039-183A-4 (1-399) x ACA34860
                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated CC nucleic acid; (3) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense CC proliferation or the activity of a gene in an operon required for producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of gene product or that has an activity against a biological pathway (2) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent compound acts; (9) identifying the target of a compound that inhibits the gene conduct is overexpressed or underexpressed; (12) determining the extent compound that inhibits in which the gene conduct is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or (13) identifying the target of a compound that inhibits the conduct is overexpressed or conduct is conducted accide required for cellular proliferation to isolate candidate molecules for rational conductions or creations or creations or creations or creations. The present is one 
                                                                                                                                                                                                                                                                                                                                                                                                                                                         K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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25-OCTI-2001; 2001US-0342923.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                      This DNA sequence codes for a 50 kDa Helicobacter pylori polypeptide (see CR AAW73035) designated GHPO 750. A polypucleotide encoding GHPO 750 can be CC obtained from genomic DNA by PCR amplification (see AAV07971-72. The CC invention provides polypucleotides (see AAV72001, AAV07912-21 and CC AAV07963-64) encoding a family 76 kDa Helicobacter polypeptides (see CAAV73022-32), GHPO 750 and a 32 kDa polypeptide (see AAW73034). These CC polynucleotides were initially identified in a search of H. pylori CC genomic databases. DNA cassettes for expression of the Helicobacter CC proteins (unprocessed or mature forms) in prokaryotic or eukaryotic cells CC are provided. The polynucleotides can be used in vacciness to prevent or treat Hb infection in a mammal. Viral (especially poxvirus) or bacterial CC vectors are used. Products and methods of the invention allow treatment CC and prevention of gastroduodenal diseases associated with Hb infections, CC diseases, e.g. gastric and duodenal ulcers. Diagnostic and detection controlled. GHPO 750 was demonstrated to be a protective anticon are also provided. GHPO 750 was demonstrated to be a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
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ACA30274

1258

Prokaryotic 19-JUN-2003 ACA30274;

design;

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the 6213 antisence sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated concluded are: (6) polypeptide or its fragment whose expression is inhibited by the antisense concluded acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular contiferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway conceptived for proliferation, or that inhibits cellular proliferation; (8) compound that influences the activity of configuration of the biological pathway in which a proliferation, or that inhibits cellular proliferation of a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of a compound's activity; (11) a culture comprising strains in which the gene cor a gene on which the test compound that inhibits proliferation of a compound's activity; (11) a culture comprising strains in which the gene cor dentifying proteins or screening for homologous nucleic acids are useful for cellular proliferation in collate candidate molecules for rational corequired for proliferation in collate candidate molecules for rational configuration. The process that candidate molecules colds required corequired for proliferation in cells other than S. aureus, S. typhimurium, colling the target of a compound that inhibits the proliferation of the proliferation in cells other than S. aureus, S. typhimurium, colling the process of the target of a compound that inhibits acids are useful acids.
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 18144; 1766pp; English.
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pneumoniae or P. acruginosa. The present sequence is one of the target okaryotic essential genes. Note: The sequence data for this patent did t form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense nucleic acids, useful for identifying proteins or a homologous nucleic acids required for cellular proliferation late candidate molecules for rational drug discovery programs
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAAB1453 to AAAB2444 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAAB1260 to AAAB1303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAAB1254 to AAAB1259 and AAAB1304 to AAAB13121 represent PRC primers used in the isolation of Neisseria meningitidis DNA sequences; and AAAB1222 to AAAB1452 represent Neisseria meningitidis DNA sequences; and AAAB1222 to AAAB1452 represent Neisseria meningitidis MenB polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification;
                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which can be in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.
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30-APR-1999;
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yGlyArgHis]	TACTATCACTATCACTA	::: cagctacatco pvalPheSer1 ccffffcco ccffffcco	uPheProGlyJ; : CTTCCCCGGCC aLysAlaGlyJ; TGCCGCT	serArgGlnV see GGCCGCCAAC pAspGlnGluI CGATGCCGAGC	CGCTGCAAAAA FILEALATHES CATTAATACCT CATTAATACCT CCCGGGGCACAC CCCGGGGGCACAC ALICLE CATTAATACCT AATCCTGGTAT
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GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr	261 ValThrGlyValGlumer PheArgLysGluLeuGluLysGlyGluLlaGlyAspAsnVal 261 ValThrGlyValGlumer PheArgLysGluLeuGluLysGlyGlyAspAsnVal	50171 TTGGACAGCTACATCCCGACTCCCGAGCGAGCCGTGGACAAACCGTTCCTGCTGCCTATC 221 GluaspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly [161 TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu 180	LeuLeuSerArgGlnValGlyValProHisIleValValPheLeuAsnLysGlnAspMet :::	GGTGGCGCTGCAAAAGCTTATGACCAAATCGACAAGCGCTCCTGAAGAAAAGCTCGTGGT 49765 IleThrIleAlaThrSerHisIleGluTyrGluThrGluAsmArgHisTyrAlaHisVal 80 ATTACCATTAATACCTCAACGTAGAATACGAAATCGAAACCCGACACACGTA 49825 AspCYsProGlyHisAlaAspTyrVallysAsmArcTGAAACCCGCCACACACGTA 49825
rgProGlnPhe	ysglyGluAla Ascilliani AAGTATACGTA AAGTATACGTA AAGTATACGTA	:: ACAAACCGTTC ACAAACCGTTC ALThrGlyArg	lySerAlaled	alPheLeuAsn	
TyrvalargThz	GGAGGAAAGG	::: : CTGCTGCCTAX IleGluArgG ::: GTAGAGCGCG GTAGAGCGCGCG GIn[ArgAlaLeuG	LysGlnAspMe	AAAGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG
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Best Local Similarity:
Query Match:
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                               US-10-039-183A-4 (1-399) x AAF21544
                                                                                                                                                      Alignment
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08-OCT-1999;
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Masignani V, Galeotti C, Mora M,
Rappuoli R, Frazer CM, Grandi G;
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                                                                   ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp
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                                       Pred. No.:
                                                           Alignment Scores
                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia (CC life themselves are the encoded proteins. The prokaryotes used are Escherichia (CC life themselves are used a Entercocccus faecalis. The invention is also (CC useful for the identification of potential new targets for antibiotic (CC development. The antisense nucleic acids can also be used to identify (CC proteins used in proliferation, to express these proteins, and to obtain (CC antibodies capable of binding to the expressed proteins. The proteins can (CC be used to screen compounds in rational drug discovery programmes. The continense nucleic acids which are required for cell proliferation in a wide variety (CC of organisms. The present sequence encodes an essential prokaryotic (CC cellular proliferation protein. Note: The sequence data for this patent (CC did not form mark of the notion).
   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-0191078P.
23-MAY-2000; 2000US-020648P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NCV-2000; 2000US-025625P.
27-DEC-2000; 2000US-0257931P.
16-PEB-2001; 2001US-0269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides antibiotics, compris
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P-PSDB; AAU33391.
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                                                                                                                             not form part of the printed specification, ctronic format directly from WIPO at .wipo.int/pub/published_pct_sequences
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the 5213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense conclusic acid; (2) a host cell containing the vector; (3) an isolated converge to the polypeptide or its fragment whose expression is inhibited by the converge to the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular converge to polypeptide; (5) producing the polypeptide; (6) inhibiting cellular converge to polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway converged for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a converge product is overexpressed or underexpressed; (12) determining the extent
                                                                                                                                                                                                                                                                                                                                                                Wang
Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                           WPI;
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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GluaspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
                                                         ValAspAlaTyrI1eProThrProGluArgAspThrGluLysThrPheLeuMetProVal
                                                                                                                            ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuSerAla
                                                                                                                                                                                                                                                                                                                            LeuLeuSerArgGlnValGlyValProHisIleValValPheLeuAsnLysGlnAspMet
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                                                                                                           GGCGACGAGTCT-----TATGAAGAAAAATCTTAGAATTAATGGCTGCA
                                                                                                                                                                                       TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu
                                                                                                                                                                                                                                          GGAGCTATCTTAGTAGTTTCTGCTGCTGATGGTCCTATGCCTCAAACACGTGAACATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspCysProGlyHisAlaAspTyrValLysAsnMetIleThrGlyAlaAlaGlnMetAsp
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1608.00
87.25%
77.00%
78.71%
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GAAGACGTATTCTCAATCACTGGACGTGGTACTGTTGCTACAGGCCGTGTTGAACGTGGT

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAACGTTGCTATGGACGTTGAATTAATTCACCCAATCGCTATCGAAGACGGAACTCGT
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                                                                                                                                                                                                                                                                                                                     antimicrobial; microbial disease; drug composition; vaccine; infection; antibacterial; food preservative.
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           2002US-0423875P.
2002US-0424362P.
2002US-0424367P.
2002US-0424370P.
2002US-0424376P.
2002US-0424376P.
2002US-0424376P.
2002US-0424389P.
2002US-0424502P.
2002US-0424664P.
2002US-0424665P.
2002US-0424665P.
2002US-0424968P.
2002US-0424968P.
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2002US-0423791P.
2002US-0423832P.
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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria. Specifically, it refers to recombinant proteins derived from Staphylococcus aureus, Helicobacter pylori, Streptococcus pneumoniae, Escherichia coli, Enterococcus faccalis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulator for the prevention or treatment of microbial diseases. Furthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccine. Accordingly, such compositions can be useful for treating bacterial infections, developing antibacterial agents useful as food preservatives or treating food products to eliminate potential pathogens. This polymucleotide sequence is a bacterial DNA encoding a protein target of the invention.
                                                                                                                                                                                                                                                                                                                                                                          Edwards A, onsoury K, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2003;
14-MAR-2003;
14-MAR-2003;
14-MAR-2003;
14-MAR-2003;
17-MAR-2003;
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08-NOV-2002

08-NOV-2002

12-MAR-2003

12-MAR-2003

11-MAR-2003

11-MAR-2003

11-MAR-2003

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11-MAR-2003

11-MAR-2003

11-MAR-2003

11-MAR-2003
                                                                                                                                                                                                                                           Claim 28;
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                                                                                                                                                                                                                                                                               Bacterial polypeptide composition useful for treating bacterial infection, has isolated, recombinant bacterial polypeptide such as chindren protein Era from Pseudomonas aeruginosa or adenylosuccinate
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P-PSDB; ADO25366.
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Pinder B,
Buzadzija
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2002US-0425201P.
2003US-0453914P.
2003US-0454123P.
2003US-0454123P.
2003US-0454215P.
2003US-0454215P.
2003US-0454215P.
2003US-0454215P.
2003US-0454215P.
2003US-0454507P.
2003US-0454507P.
2003US-0455036P.
2003US-0455036P.
2003US-0455034P.
2003US-04553343P.
2003US-04553343P.
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Alam MZ, 1
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Sequence 1185 BP; 376 A; 235 ü 254 G; 320 T; 0 U; 0 Other;

S Percent Similarity:
Best Local Similarity:
Query Match: ঠ 용 Score: US-10-039-183A-4 (1-399) x ADO25365 21 ValAspHisGlyLysThrThrLeuSerAlaAlaIleSerAlaValLeuSerLeuLysGly MetAlaLysGluLysPheAsnArgThrLysProHisValAsnIleGlyThrIleGlyHis ATGGCAAAAGAAAATTTGACCGTTCTAAATCCCATGTTAACATTGGTACTATCGGACAC 1.64e-148 1608.00 87.25% 77.00% 78.71% (1-1185)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

61

GTTGACCATGGTAAAACTACATTAACAGCTGCAATTGCTACTGTATTATCAAAACACGGT

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1126
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ThrThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGly
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                                                                                                          AspAsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLys
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US-10-039-183A-4 (1-399) x AAS52748

MetAlaLysGluLysPheAsnArgThrLysProHisValAsnIleGlyThrIleGlyHis

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(1-1188)

Gaps:

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                    Alignment
                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, CC their use in the discovery of novel antibiotics, the essential genes CC themselves and the encoded proteins. The prokaryotes used are Escherichia CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also CC useful for the identification of potential new targets for antibiotic CC development. The antisense nucleic acids can also be used to identify CC proteins used in proliferation, to express these proteins. and to obtain CC antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The cantisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety CC of organisms. The present sequence encodes an essential prokaryotic CC cellular proliferation protein. Note: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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P-PSDB; AAU34889.
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                                                    ACAACAGACGTTACTGGTGTTGTAGAATTGCCAGAAGGTACTGAAATGGTAATGCCTGGT
                                                                         ThrThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGly
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression cc of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense culticacid; (2) a host cell containing the vector; (3) an isolated cc nucleic acid; (2) a host cell containing the vector; (3) an isolated cc polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required conjudication in cells other than S. aureus, S. typhimurium,
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

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Frazer CM, I
Masignani V,
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CC AA81260 to AA81303 and AAB25620 to AA81561 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AA81259 and
CC AA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MenB polynuclectide ORF sequences, which are all
CC Used in the exemplification of the present invention. The nucleic acid
CC the manufacture of a composition. The composition can be used in
CC the manufacture of a composition. The composition can be used in
CC cexample, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neissariae. Identification of sequences from the bacterium
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC antigenically variable or at least more conserved than other more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65632 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rappuoli
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n Neisseria genomic sequences. AAA81453 to AAA82414 represent
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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria. Specifically, it refers to recombinant proteins derived from Staphylococcus aureus, Helicobacter pylori, Streptococcus pneumoniae, Escherichia coli, Enterococcus faccalis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulator for the prevention or treatment of microbial diseases. Furthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccine. Accordingly, such compositions can be useful for treating bacterial infections, developing antibacterial agents useful as food preservatives or treating food
                                                                                                                                                                                                                                                                                                                                                                                  Mansoury K, Mcdonald M,
                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                               Bacterial polypeptide composition use infection, has isolated, recombinant binding protein Era from Pseudomonas from Enterococcus faecalis.
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Search completed: April 24, 2005, 06:16:41 Job time: 917.259 secs

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-DB=Issued_Patents NA -OFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER-US10039183 @CGN 1 1 219 @runat 22042005 122426 20141 -NCPU=6 -ICPU=3
-NO MPAP -LARGEQÜERY -NEO_SCORES=0 -WAIT -DSPEIJCNE170 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
                                                                                                              Score:
US-10-039-183A-4 (1-399) x US-09-902-540-8380
                                                    Query Match:
                                                                                                                               Pred. No.:
                                                                                                                                              Alignment Scores:
                                                                                                                                                                                 US-09-902-540-8380
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                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8380
LENGTH: 1191
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8380, Applic
Patent No. 6833447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8380, Application US/09902540 o. 6833447
                                                    2.12e-171
1585.50
86.50%
75.75%
                                                      Conservative: Mismatches: Indels:
                                                                                                            Length:
Matches:
   (1-1191)
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PheAlaIleArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu
                               GACAACATCGCCATCGAGGTGGAGCTCATCACCCCCGTGGCCATGGAGAAGGAGCTGCGC
                                            AspAsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLys
                                                                                              ACCACGGACGTGACGGCTCGGTGAAGCTGCCGGAGAACGTCGAAATGGTGATGCCGGGC
                                                                                                               ThrThrAspValThrG1ySerIleThrLeuProG1uG1yValG1uMetValMetProG1y
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegand, Roger C.
APPLICANT: Miegand, Roger C.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: unsure
; LOCATION: (1)..(703
; OTHER INFORMATION:
US-09-902-540-878
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; LENGTH: 7035
; TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 3
US-08-743-637B-185
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GENERAL INFORMATION:
APPLICANT: BERGER
APPLICANT: PICARD
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 185, Application US/08743637B
                                                                                                                                                                                       APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PACHOGENS AND ASSOCIATED

TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

NUMBER OF SEQUENCES: 273

CORRESPONDENCE: CARDEES:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                            STREET: 411 EAST I
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
                                                                                                                                                                              ADDRESSEE:
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411 EAST WISCONSIN AVENUE
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OUELLETTE, Marc
ROY, Paul H.
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Best Local Similarity:
Query Match:
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TELEPAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 base pairs
TYPE: nucleic acid
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,84
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REGISTRATION NUMBER: 35,433
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
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ORIGINAL SOURCE:
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TOPOLOGY: linear
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                                                               TATGACTTCCCAGGTGACGATACACCAATCGTACGTGGTTCAGCATTACAAGCGTTA---
                                                                                  TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu
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Conservative:
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RESULT 4
US-09-557-884-1
; Sequence 1, Application US/Uyzzzz;
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: Fleischmann et al.
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
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               APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genon
STREET: 9410 Key West
CITY: Rockville
                                                                                                                                   SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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    REGISTRATION
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   NUMBER: 41,971
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SEQUENCE CHARACTERISTICS:
HEAGHT: 1830121 base partype: nucleic acid
STYPE: nucleic acid
STRANDEDNESS: double
HOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ II
US-09-557-884-1
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Best Local Similarity:
Query Match:
DB:
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TELECOMMUNICATION INFORMATION:
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ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr
                                                             GluAspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
                                                                                                                                                                                 GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
                                                                                                                                                                                                                          TATGACTTCCCAGGTGACGATACACCAATCGTACGTGGTTCAGCATTACAAGCGTTA---
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                                               GAAGATGTGTTCTCAATCTCAGGTCGTGGTACTGTAGTAACAGGTCGTGTAGAACGAGGT
                                                                                                         -----AACGGCGTAGCAGAATGGGAAGAAAAATCCTTGAGTTAGCAAACCAC
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Conservative:
Mismatches:
Indels:
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: the Nucleotide sequence of the Haemophilus influenzae
Thereof, and Uses Thereof
                                                                             APPLICATION MUMBER: 08/476,102
APPLICATION MUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REPERENCE/DOCKET NUMBER: PB18693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8504
TELEPAX: 301-309-8504
TELEPAX: 301-309-8504
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text
 SEQUENCE
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/557,884
PILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                TYPE: nucleic acid
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STATE: MD
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                  STRANDEDNESS: double TOPOLOGY: linear
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DESCRIPTION: SEQ ID NO:
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ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu 320
                                                     GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
                                                                                                                                                                                                                                                                                                                                                                                                             GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAGATGACGAAGAGTTATTAGAATTAGTCGAAATGGAAGTTCGTGAACTTCTATCTCAA 596603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuSerAla
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                                   GGTGCATTATTACGTGGTACCAAACGTGAAGAAATCGAACGTGGTCAAGTATTAGCGAAA
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GENERAL INFORMATION:
                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION NOTA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: «Unknown»
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                                                                                                                                                                                            NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEFHONE: 301.610-5790
TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert D.
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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J. Craig Venter
J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae
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                                                                        ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu 320
                                                                                                                GGTGCATTATTACGTGGTACCAAACGTGAAGAAATCGAACGTGGTCAAGTATTAGCGAAA
                                                                                                                                   GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
                                                                                                                                                                                GTAACGGGTGTTGAAATGTTCCGTAAATTACTTGACGAAGGTCGTGCAGGTGAAAACATC
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RESULT 7
US-09-643-990A-1/c
; Sequence 1, Application U
; Patent No. 6528289
; Patent No. 6528700;
; GENERAL INFORMATION:
          Percent Similarity:
Best Local Similarity:
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                                                                                                                       ; SEQUENCE DESCRIPTION: SEQ US-09-643-990A-1
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                                                                 Score:
                                                                                          Alignment Scores:
                                                                                                                                                                       NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
                                                                                No.:
                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
PILING DATB: 23-Aug-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
PILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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COUNTRY: USA
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INVENTION: The Nucleotide sequence of
the Haemophilus influenzae
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Matches:
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ACAGACGTGACTGGTACAATCGAATTACCAGAAGGCGTGGAAATGGTAATGCCAGGCGAT
                                                    ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu 320
                                                                                                                                                                 GGTGCATTATTACGTGGTACCAAACGTGAAGAAATCGAACGTGGTCAAGTATTAGCGAAA
                                                                                                                                                                                GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
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           ThraspValThrG1ySerIleThrLeuProGluG1yValGluMetValMetProG1yAsp
                                                                                                                                                                                                                       GTAACGGGTGTTGAAATGTTCCGTAAATTACTTGACGAAGGTCGTGCAGGTGAAAAACATC
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US-09-134-001C-2540
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APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2540
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Patent No. 6380370
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                                                                                                                           GENERAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Kallender, Stephanie
TITLE OF INVENTION: EF-Tu
FILE REFERENCE: GM10185
CURRENT APPLICATION UNMBER: US/09/218,197A
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1185
Percent Similarity:
Best Local Similarity:
Query Match:
                                       Score:
                                                                                         ; TYPE: DNA
; ORGANISM: SI
US-09-218-197-1
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US-09-218-197-1
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ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp 360
                                                                      CCTGGTTCAATTACACCACATACTGAATTTAAAGCAGAAGTATACGTATTATCAAAAGAC
                                                                                  GTTACAGGTGTTGAAATGTTCCGTAAATTATTAGACTACGCTGAAGCTGGTGACAACATT
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Percent Similarity:
Best Local Similarity:
Query Match:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ
US-08-956-171E-82
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US-10-039-183A-4 (1-399) x US-08-956-171E-82 (1-15598)
                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ETELECOMMUNICATION INFORMATION: TELEPHONE: (240) 314-1224
TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb stc

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTMARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION DATA:

CLASSIFICATION LOWBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION CHARACT

CLASSIFICATION NUMBER: 60/009,861

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

TREGISTRATION NUMBER: 46,789
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Michael R. Fannon
TITLE OF INVENTION: Staphylococcus
NUMBER OF SEQUENCES: 5256
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Gil H. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1066
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STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                   LENGTH: 15598 base pairs
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Patrick S. Dillon
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GluAspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
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                                                                                                               ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp
                                                                                                                                                                        GAAGGTGGACGTCACACTCCATTCTTCTCAAACTATCGTCCACAATTCTATTTCCGTACT
                                                                                                                                                                                                          GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr 340
                                                                                                                                                                                                                                                                   CCTGGTTCAATTACACCACATACTGAATTCAAAGCAGAAGTATACGTATTATCAAAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGACGATGAAGAATTATTAGAATTAGTAGAAATGGAAGTTCGTGACTTATTAAGCGAA 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuSerAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTTATCACGTAACGTTGGTGTACCAGCATTAGTAGTAGTATTCTTAAACAAAGTTGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAlaIleLeuValValSerAlaAlaAspGlyProMetProGlnThrArgGluHisIle 120
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Percent Similarity:
Best Local Similarity:
Query Match:
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 15598 base pairs
TYPE: nucleic acid
TYPE: nucleic double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-781-986A-82
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                                                                                                                                                                                                                                                                                       US-10-039-183A-4 (1-399) x US-08-781-986A-82 (1-15598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 82, Application US/08781986A Patent No. 6737248
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APPLICANT: Charle
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NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Staphylococcus
NUMBER OF SEQUENCES: 5255
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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IleThrIleAlaThrSerHisIleGluTyrGluThrGluAsnArgHisTyrAlaHisVal
                                                                                             LeuAlaGluMetLysAspTyrAspAsnIleAspAsnAlaProGluGluLysGluArgGly
                                                                                                                                                                            ValAspHisGlyLysThrThrLeuSerAlaAlaIleSerAlaValLeuSerLeuLysGly
                                                                                                                                              GTTGACCATGGTAAAACAACATTAACAGCAGCAATCGCTACTGTATTAGCAAAAAATGGT
                                                                         GACTCAGTTGCACAATCATATGACATGATTGACAACGCTCCAGAAGAAAAAAAGAACGTGGT
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86.47%
74.19%
76.92%
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 28, Application US/0959600
Patent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SI
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US-09-596-002-28
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------GGCGATGCTCAATACGAAGAAAAATCTTAGAATTAATGGAAGCT 12119
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                                                                                                                                                        TCAATCCGTGAAGGTGGACGTACTGTAGGATCAGGCGTTGTTACTGAAATCATTAAA
                                                                                                                                                                   AlaIleArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu 399
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   NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
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Best Local Similarity:
Query Match:
DB:
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; OTHER INFORMATION: Incyte template
; PUBLICATION INFORMATION:
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SEQ ID NO 28
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CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
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ORGANISM: M. catarrhalis
FEATURE:
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                                                 ACACTAGACAGCTATATCCCCAGAGCCTGAGCGTGATATCGATAAGTCATTCTTGATGCCA
                                                                 GluValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetPro
                                                                                                                                     GluAlaLysAlaGlyAsnValGlyGluTrpGlyGlu---LysValLeuLysLeuMetAla
                                                                                                                                                                                                                                                                                                             LeuLeuSerArgGlnValGlyValProHisIleValValPheLeuAsnLysGlnAspMet
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                                                                                                           -----GGTTCTGATGGTAAATATGGCGAGCCTGCAGTTCTAGAACTGCTAGAC
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Sequence 86, Application US/09492709A

Patent No. 6720139

GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Cyskind, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Wamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001A
CURRENT APPLICATION NUMBER: US/09/492,709A
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-492-709A-86
                                        US-10-039-183A-4 (1-399) x US-09-492-709A-86 (1-1185)
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                                                                                                                                                SEQ ID NO 86
LENGTH: 1185
TYPE: DNA
ORGANISM: E. Coli
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                                                             ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp
                                                                                                     GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr 340
                                                                                                                               CCGGGCACCATCAAGCCGCACACCAAGTTCGAATCTGAAGTGTACATTCTGTCCAAAGAT
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            AACATCAAAATGGTTGTTACCCCTGATCCACCCGATCGCGATGGACGACGGTCTGCGTTTC
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton of
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3648
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               GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
                                                                                                     ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuSerAla 160
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                                                                                         GTTGATGACGAAGAGCTGCTGGAACTGGTTGAGATGGAAGTTCGTGAACTGCTGTCTCAG
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MetAlaLysGluLysPheAsnArgThrLysProHisValAsnIleGlyThrIleGlyHis
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Percent Similarity:
Best Local Similarity:
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US-09-489-039A-3750/c
US-10-039-183A-4 (1-399)
                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                           APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT FILING NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3750
LENGTH: 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3750, Application Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLysPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGGCACCATCAACCCGCACACCAACTTCGAATCTGAATGTACATCCTGTCCAAAGAC
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1555.50
85.18%
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x US-09-489-039A-3750 (1-1260)
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380 76	361 AsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLysPhe 3 ::: ::: :::
360 136	341 ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp
340 196	321 GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr
320 256	301 ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu :::
300 316	281 GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
280 376	261 ValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnVal
260 436	241 ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr :::::: :::
240 496	221 GluAspvalPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
220 556	201 ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal :::
200	181 GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
	161 TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu :::
160 721	141 ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuSerAla :::
140 781	121 LeuLeuSerArgGlnValGlyValProHisīleValValPheLeuAsnLysGlnAspMet
120 841	101 GlyAlaIleLeuValValSerAlaAlaAspGlyProMetProGlnThrArgGluHisIle
901	81 AspCysProGlyHisAlaAspTyrValLysAsnMetIleThrGlyAlaAlaGlnMetAsp
961	61 IleThrIleAlaThrSerHisIleGluTyrGluThrGluAsnArgHisTyrAlaHisVal
60 1021	41 LeuAlaGluMetLysAspTyrAspAsnIleAspAsnAlaProGluGluLysGluArgGly ::: :::
	21 ValasphisGlyLysThrThrLeuSerAlaAlaIleSerAlaValLeuSerLeuLysGly
1141	1200 GTGTCTAAAGAAAATTTGAACGTACAAAACCGCACGTCAACGTTGGTACTATCGGCCAC

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75 GCAATCCGTGAAGGCGGCCGTACCGTTGGCGCGGGCGTTGTAGCTAAAGTTCTG 22	381 AlaileArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIle 398
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Search completed: April 24, 2005, 12:23:55 Job time : 2662.22 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Q-(cgn2 1)(USPTO_spool)(USIO39183/runat_22042005_122426_20167/app_query.fasta_1.1038-Q-(cgn2 1)(USPTO_spool)(USIO39183/runat_22042005_122426_20167/app_query.fasta_1.1038-DB-Published_Applications_NA_QFMT=fastap_SUFFIX=rnpb-MINMATCH=0.1
-LOOPEXI=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
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-MODEL=frame+_p2n.model
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                                                                                                                              /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,

SUMMARIES

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sequence 4519, Ap Sequence 115, App Sequence 8344, Ap Sequence 7572, Ap Sequence 240, Appl Sequence 19, Appl Sequence 82, Appl Sequence 82, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 32228, A Sequence 26722, A	sequence 1, App Sequence 35489, Sequence 12928, Sequence 34285, Sequence 31070, equence 1, Appli	24743, 29207, 14613, 14772, 962, Ap 2720, Ap 22060, 1, App 1, App 1, App	ַלְּיִלְיִלְיִילְיִלְיִילְיִלְיִילְיִלְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְיִילְי	Description

ALIGNMENTS

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RESULT 1
US-09-815-242-7318
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                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                   Wall, Daniel
                                                                                                                                                                                                          Carr, Grant J.
                                                                                                                                                                                                                                Trawick, John D.
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-2-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-0
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Query Match:
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ORGANISM: Helicobacter p:
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1200)
JS-09-815-242-7318
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RESULT 2
US-10-282-122A-22730
US-10-282-122A-22730, Application US/10282122A
Sequence 22730, Application US/10282122A
publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Gerr, Grant
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE CORT INVENTION: Identification of Essential Ge FILE REFERNCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR PRIOR APPLICATION data removed - See
NUMBER OF SEQ ID NOS: 78614
SOPTWARE: Patentin version 3.1
SEQ ID NO 22730
LENGTH: 1200
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; ORGANISM: Helicobacter pylori
US-10-282-122A-22730
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Best Local Similarity:
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Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding INVENTION: BEDUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                         CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versic
SOFTWARE: FastSEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
ATTONNEY/ACENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/03700
TELEPHONE: 617-428-0200
                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1448 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                              TELEPHONE: 617-428-02
TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                 Version
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Polynucleotides

1080 360

340

960 320 900 300

840

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; MOLECULE TYPE: Genomic I
; FEATURE:
; NAME/KEY: Coding Seque
; LOCATION: 118...1314
; OTHER INFORMATION:
US-08-831-310-3
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                      ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal
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                                                                                                 GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
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Matches:
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D	<u> </u>	Alignme Pred. N Score: Percent Best Lo Query M DB:	ns-1	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		RESU US-1 ; Se ; Pu ; GE	g Q	д Q	D Qy	Db Qy	g Q	gb Qy
CAAAAGAAAAGTTTAACAGAACTAAGCCGCATGTTAATATTTGGAACCATTGGCAT	0-039-1	Alignment Scores: Pred. No.: \$2043.00	LENGTH: 1448 TYPE: DNA ORGANISM: Helicobacter pylori FEATURE: NAME/KEY: CDS LOCATION: (118)(1314)	CURRENT APPLICATION NUMBER: US/10/039,183A CURRENT FILING DATE: 2002-12-13 CURRENT PAPLICATION NUMBER: US 08/831,310 PRIOR APPLICATION NUMBER: US 08/831,310 PRIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 18 SOFTWARE: FastSEQ for Windows Version 4.0	APPLICANT: Lissolo, Ling APPLICANT: Lissolo, Ling APPLICANT: Tomb, Jean-Francois APPLICANT: Miller, Charles APPLICANT: Al-Garawi, Amal TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750 TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules FILE REPRENCE: 06132/077002	RESULT 4 US-10-039-183A-3 ; Sequence 3, Application US/10039183A ; Publication No. US20030143242A1 ; GENERAL INFORMATION: Applicant. Kleanthous, Harold	381 AlaileArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu 399 	361 ABNVALLYBI1eThrValGluLeuI1eSerProValAlALeuGluLeuGlyThrLyBPhe 380 	341 ThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp 360 	321 GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr 340 	301 ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu 320 	281 GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys 300

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RESULT 5
US-10-662-126-32
; Sequence 32, Application US/10662126
; Publication No. US20050063987A1
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                                                                                                    AlaIleArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu
                                                                                                                                                                                                                                                                                             GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr
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                                                                                                                                                  AATGTGAAAATCACTGTAGAGTTGATTAGCCCCTGTTGCGTTAGAGTTGGGAACTAAATTT
                                                                                                                                                                     AsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLysPhe
                                                                                                                                                                                                                ACTGATGTGACTGGCTCTATCACCCTTCCTGAAGGCGTAGAAATGGTTATGCCTGGCGAT
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CURRENT APPLICATION NUMBER: US/10/662,126

CURRENT FILING DATE: 2003-09-12

PRIOR APPLICATION NUMBER: 09/230,158

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: POT/IB97/00981

PRIOR FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 32

LENGTH: 2825

TYPE: DNA

ORGANISM: Helicobacter pylori

PEATURE:
NAME/KEY: CDS

LOCATION: (891)..(2090)

OTHER INFORMATION: bp protein; 42 kD protei
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APPLICANT: Knapp, Bernhard
APPLICANT: Hundt, Erika
APPLICANT: Schmidt, Karl-Heinz
APPLICANT: Schmidt, Karl-Heinz
TITLE OF INVENTION: Proteins, In Particular Membrane Proteins, of
TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use
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                                                     TATGAATTCCCTGGTGATGACACTCCTATCGTAGCGGGTTCAGCTTTAAGAGCTTTAGAG
                                                                      TyrGluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu
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Sequence 18144, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Jamudio, Carlos
APPLICANT: Jamudio, Carlos
APPLICANT: Zamudio, Cheryl
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
ITITLE OF INVENTION: Identification of Essential Genes in Malone of Invention NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/2030,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,337

PRIOR APPLICATION NUMBER: 60/230,337
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SEQ ID NO 18144
LENGTH: 1200
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRIOR PRIOR 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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                                                 ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal
                                                                                                TATGATTTCCCAGGCGATGATACACCTATTATTTCTGGTTCTGCTTTAAAAGCTCTTGAA
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/101,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3832
LENGTH: 1185
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Patent No. US30020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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Sequence 6275, Application US/10282122A

| Publication No. US20040029129A1
| GENERAL INFORMATION:
| APPLICANT: Wanng, Liangsu
| APPLICANT: Zamudio, Carlos
| APPLICANT: Haselbeck, Robert
| APPLICANT: DAlsen, Kari
| APPLICANT: Malone, Cheryl
| APPLICANT: Wall, Daniel
| APPLICANT: Trawick, John
| APPLICANT: Wall, Daniel
| APPLICANT: Yamamocto, Robert
| APPLICANT: Yamamocto
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US-10-282-122A-6275
                                                                     US-10-282-122A-6275
                                                                                 SEQ ID NO 6275
LENGTH: 1185
TYPE: DNA
ORGANISM: Enterococcus
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SOFTWARE: PatentIn version 3.1
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                                                                                                                     ValGlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCys
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. — 4	Qy 1 MetAlaLysGluLysPheAsnArgThrLysProHisValAsnIleGlyThrIleGlyHis 20	-815-2	Mismaccnes: Indels: Gaps:	Fred. NO.: 4.92e-145 Length: 1188 Score: 1608.00 Matches: 308 Percent Similarity: 87.25% Conservative: 41	Scores:	; NAME/KAX: CDS ; LOCATION: (1)(1188) US-09-815-242-6385	; TYPE: DNA ; ORGANISM: Enterococcus faecalis ; FEATURE:) NUMBER OF SEQ ID NOS: 14110 ; SOPTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 6385 ; LENGTH: 1188	; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/269,308 ; PRIOR FILING DATE: 2001-02-16	; PRIOR FILING DATE: 2000-11-27 ; PRIOR APPLICATION NUMBER: 60/257,931	; PRIOR APPLICATION NUMBER: 60/242,578 ; PRIOR FILING DATE: 2000-10-23 ; PRIOR APPLICATION NUMBER: 60/253,625	; FRIOR RILING DATE: 2000-05-23 ; PRIOR RILING DATE: 2000-05-26 ; PRIOR FILING DATE: 2000-05-26	; PRIOR APPLICATION NUMBER: 60/191,078 ; PRIOR FILING DATE: 2000-03-21	CURRENT FILING DATE: 2001-03-21	APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes PTLE BEREFERNOR: FITTED 0113	; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J. ; APPLICANT: Yamamoto. Robert T.	GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Zyskind, Judith W.	RESULT 9 US-09-815-242-6385 / Sequence 6385, Application US/09815242 / Patent No. US20020061569A1	Qy 380 PheAlaIleArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu 399 ::: ::: :::: Db 1126 TTCTCTATTCGTGAAGCGGACGTACTGTAGGTTCAGGCGTTGTTACTGAAATCGTTAAA 1185		1006 ACAACAGACGTTACTGTTGTAGAATTGCCAGAAGGTACTGAAATGGTAATGCCTGGT	340	946 GAAGAAGGCGGACGTCACACTCCATTCTTCACTAACTACCGTCCTCAATTCTACTTCCGT 1005
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420 140 360 120 300 100 240 80

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APPLICANT: Wallow:
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yamanoto, Robert
APPLICANT: Young Darie: 1001-02-02-02
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/243,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09
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Best Local Similarity:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Zamudio, Carlos
AspCysProGlyHisAlaAspTyrValLysAsnMetIleThrGlyAlaAlaGlnMetAsp
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Zyskind, Judith
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Malone, Cheryl
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 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
                                                                                            Sequence 29230, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
FIITE OF INVENTION: Identification of Essential Genes in Internation NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 29230
LENGTH: 1182
TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
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                                   GlyAlaIleLeuValValSerAlaAlaAspGlyProMetProGlnThrArgGluHisIle
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                                                                                                                                                   IleThrIleAlaThrSerHisIleGluTyrGluThrGluAsnArgHisTyrAlaHisVal
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           Sequence 11657, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, Robert
APPLICANT: Trawick, Robert
APPLICANT: Trawick, Robert
APPLICANT: Forsyth, R.
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Yamamoto, Rc
Forsyth, R.
Xu, H.
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TYPE: DNA
; ORGANISM: Burkholderia cepacia
US-10-282-122A-11657
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11657
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OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                            Zyskind, Judith Wall, Daniel Trawick, John Carr, Grant Yamamoto, Robert Forsyth, R.
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
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; ORGANISM: Burkholderia
US-10-282-122A-14300
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FILING DATE: 2000-09-06
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GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and
FILE OF INVENTION: Listeria innocua, genome and
FILE OF INVENTION: Listeria innocua, genome and
FILE OF INVENTION: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PATENTIN VETRION 3.0
SEQ ID NO
SEQ ID NO
SEQ ID NO
  Alignment Scores: Pred. No.:
                                                                  US-10-398-221-9
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US-10-398-221-9
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Publication No. US20040018514A1
                                                                                       NAME/KEY: misc_feature LOCATION: (1)..(end) OTHER INFORMATION: n ca
                                                                                                                                                          LENGTH: 684707
TYPE: DNA
ORGANISM: Listeria innocua
FEATURE:
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319 339	300 LyseroGlyserilethrerohislyslyseheGluGlyGluileTyrValleUSerlys 3	рь 46:
o io	80 ValGlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCys	Qy 46.
279 163493	260 ThrValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsn 2	Оу Db 46
259 163433	241 ValValLyBValGlyAspGluValGluIleValGlyIleArgProThrGlnLyBThr 2	Qy Db 46:
240 463373	221 GluAspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly 2	Qу рь 46:
220 463313	201 ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal 2 :::	Оу Db 463
200 463253	181 GluAlaLysAlaGlyAsnValGlyGluTxpGlyGluLysValLeuLysLeuMetAlaGlu 2 3209	Оу Db 46
L80 163208	161 TyrGlupheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGlu 1	Оу рь 46:
L60 163148	141 ValAspAspGlnGluLeuLeuGluLeuValGluMetGluValArgGluLeuLeuScrAla 1	Оу Db 46:
L40 163088	121 LeuLeuSerArgGlnValGlyValDroHisTleValValDheLeuAsnLysGlnAspMet 1	Qy Db 46:
163028	101 GlyAlaileLeuValValSerAlaAlaAspGlyProMetProGlnThrArgGluHisIle 1	Qy Db 46:
L00 162968	81 ABPCYBProGlyHiBAlaAspTyrValLySAsnMetIleThrGlyAlaAlaGlnMetAsp 1 	Qy Db 46:
30 162908	61 IleThrileAlaThrSerHisIleGluTyrGluThrGluAsnArgHisTyrAlaHisVal 8	Оу Db 46:
50 162848	41 LeuAlaGluMetLy8AspTyrAspAsnIleAspAsnAlaProGluGluLy8GluArgGly 6 ::: :::	Оу Db 46:
10 162788	21 ValasphisGlyLysThrThrLeuSeralaalaileSeralaValLeuSerLeuLysGly 4	Qy Db 46:
20 462728	1 MetAlaLysGluLysPheAsnArgThrLysProHis	46
		Score: Percent S: Best Loca: Query Mate DB:

탕	S	D	ঠ	망	8	Db.
463794	380	463734	360	463674	340	463614
TTCTCTATCCGTGAAGGCGGACGTACAGTAGGCGCTGGCGTTGTTTCTAACATC 463847	380 PheAlaIleArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIle 397	GATAACATTGAGCTTGCAGTTGAACTAATTGCACCAATCGCTATCGAAGACGGTACTAAA 463793	360 AspAsnValLysIleThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLys 379	ACTACTGACGTAACTGGTATTGTTACACTTCCAGAAGGTACTGAAATGGTAATGCCTGGT 463733	340 ThrThrAspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGly 359	

Search completed: April 24, 2005, 12:12:39 Job time : 1087.99 BECB



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Result
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-Q-/Ggn2 1/USPTO_spool/US10039183/runat_22042005 122425 20124/app_query.fasta_1.1038
-Q-/Ggn2 1/USPTO_spool/US10039183/runat_22042005 122425 20124/app_query.fasta_1.1038
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10039183 @GCN_1 1 5533 @runat_22042005 122425 20124 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

But 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr)

Heb : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogn members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., ArabidopsIs thaliana (thale cress)

ArabidopsIs thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1617)

Castelll, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,

Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,

Menard, M., Caboche, M., Weissenbach, J. and Salanoubat, M.

Mhole Genome Sequence Comparisons and Fill-Length CDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome CNSOA2SS 1617 bp mRNA linear HTC Arabidopsis thaliana Full-length CDNA Complete sequence GSLTL656ZD02 of Adult vegetative tissue of strain col-0 Arabidopsis thaliana (thale cress): HTC 06-FEB-2004 ence from clone ol-0 of

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URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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AlaGluMetLysAspTyrAspAsnIleAspAsnAlaProGluGluLysGluArgGlyIle
                                                CTTACTGAGAATCCTAAGGTTAAGAGAGGTGAT---AACAAATGGGTAGATAAGATTTAT
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/tissue_type="Adult vegetative
/plasmid="pCMVSPORT_6"
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                                                                        Ma, I., Wangc, J., Chen, C., Liu, X., Su, Jiao, Y., Sun, N., Zhang, X., Bao, J., Su Wong, G.K.S., Deng, X.W. and Wang, J. An analysis of transcriptional regula its comparison to Arabidopsis Unpublished (2004)
Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing Tel: 86-10-80481559
Fax: 86-10-80481559
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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CGCAACTGCÁCGGTGÁCTGGTTGÁGÁTGTTCCAGÁÁGACCATGGATGATGCGATGGCT
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full Fringth
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HTC; GSLT_CDNA.
Arabidopsis thallana (thale cress)
Arabidopsis thallana
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/organism="Arabidopsis
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Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of temaize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, lowa State, then clones may be requested from ZmDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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/db_xref="MaizeDB:637696"
/db_xref="taxon:4577"
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Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; endicots; core endicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1575)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,

Menard, M., Cruaud, C., Quetier, F., Brassich, J. and Salanoubat, M.

Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

Mhole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-NOV-2003) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E. - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX827558.1 GI:
HTC; GSLT_cDNA.
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                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
    Location/Qualifiers
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                                                                                             /tissue_type="Adult vegetative /plasmid="pCMVSPORT_6" complement(1...1575)
                                                                              'gene="At4g02930"
                                                                                                                                                                            mol_type="mRNA"
|strain="Col-0"
                                                                                                                                            clone="GSLTLS73ZE07"
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GlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThrThr
                                                                        SerileAlaGlyArgGlyThrValValThrGlyArgIleGluArgGlyValValLysVal
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ACCACTTTGACTGCTGCAATCACAAAGGTTCTTGCTGAGGGGGCAAAGCTAAAGCTATT
                                GGTTCATGCAAGACATACAAGAAGTCTGAAGCAGAGATTTACGTGCTCACAAAGGATGAA
                                            GlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGluGlu
                                                                                                               ACTGGGGTTGAGATGTTCAAGAAGATCTTGGATAATGGACAGGCTGGTGATAATGTAGGA
                                                                                                                            ThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnValGly
                                                                                                                                                         GGTGAAGAAGTTGAGATATTGGGTCTACGTGACCGGGGTGTCCCACTGAAATCGACTGTA
                                                                                                                                                                     GlyAspGluValGluIleValGlyIleArgPro-----ThrGlnLysThrThrVal
                                                                                                                                                                                                                                         ATACCTGTCCCTGTTCGCGTCCTTGACAAGCCTTTCTTGATGCCAATTGAAGATGTTTTC
                                                                                                                                                                                                                                                        IleProThrProGluArgAspThrGluLysThrPheLeuMetProValGluAspValPhe
                                                                                                                                                                                                                                                                                  AsnValGlyGluTrpGlyGluLysValLeu---LysLeuMetAlaGluValAspAlaTyr
                                                                                                                                                                                                                                                                                                                           GATGATATTCCCATCATCCGAGGATCTGCTCTGTCCGCATTACAG------GGC
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
9279253
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A. Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Harata, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (Dases I to 1611)
                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamameto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K. Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki, Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of ne Genome Res. 10 (10), 1617-1630 (2000)
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1611 bp mRNA linear HTC 03-APR-Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2300002G02 product:ELONGATION FACTOR TU,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
    AspHisGlyLysThrThrLeuSerAlaAlaIleSerAlaValLeuSerLeuLysGlyLeu
                                           GCCAAGAAGACTTATGTACGCGACAAGCCCCATGTGAATGTGGGTACCATCGGACATGTG
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TREHLLLAKQIGVEHVVYVNKADAVQDSEMVELVELEIRELLTEFGYKGEETPVIVG
SALCALEQRDFELGVKSVQKLLDAVVTYIPVPTGLUKFFLLFVESVYSIPGRGTVVT
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RRGLVMVKPGSIOPHOKVEAQVYILSKEEGGRHKPFVSHFMPVMFSLTWDMACRVILE
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                             Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 1-7-22 Suehiro-cho, Yokohama 
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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TO 3-APR-200-
Mus musculus 13 days embryo heart CDNA, RIXEN full-length enriched library, clone:D330035P20 product:ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR (P43) homolog [Homo sapiens], full insert
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Kanagawa 230-0045,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   Japan (E-mail:genome-res@gsc.riken.jp,
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Please visit our web site for further details.
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CysProGlyHisAlaAspTyrValLysAsnMetIleThrGlyAlaAlaGlnMetAspGly
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SALCALEQRDPELGVKSVQKLLDAVDTYIPVTRILDKFFLLVESVYSIFGRGTVVT
GTLERGILKKGDECELLGHNKNIRTVVTGIEMFHKSLERAEAGDNLGALVRGLKREDL
RRGLVNVKPGSIQPHQKVEAQVYILSKEEGGRHKFPVSHFMPWHFSLTMDMACRVILB
RGKELAMPGEDLKLSLILRQPMILEKGQRFTLRDGNKTIGTGLVTDVPAMTEEDKNIK
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MITOCHONDRIAL PRECURSOR (P43) homolog [Homo sapiens]
(SWISSPROT P49411, evidence: FASTY, 93.8%ID, 99.7%length,
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
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db_xref="taxon:10090"
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                 HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
                                                                                CR593603 1494 bp n full-length cDNA clone CSODKOllYCO1 of Homo sapiens (human).
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned
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                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                  GluAspValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
                                                                                                              ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal
                                                                                                                                                                                  AlaLysAlaGlyAsnValGlyGluTrpGlyGluLys---ValLeuLysLeuMetAlaGlu
                                                                                                                                                                                                                                   GluPheProGlyAspAspThrProIleValAlaGlySerAlaLeuArgAlaLeuGluGlu
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                                                                                                                                                                                                                                                                                                                                          CTGGCCAGACAGATTGGGGTGGAGCATGTGGTGTGTGAACAAGGCTGACGCTGTC
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                                    GAGGCGGTGTACTCCGTCCCTGGCCGTGGCACCGTGGTGACAGGTACACTAGAGCGTGGC
                                                                                           GIGGACACTIACAICCCAGIGCCCGGGACCIGGAGAAACCCITICCIGCIGCCGGIG
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81 311 61 41

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US-10-039-183A-4 (1-399) x CR621980
                                                                                                                                                                                                                                                                                                                                                               into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
AlaLysGluLysPheAsnArgThrLysProHisValAsnIleGlyThrIleGlyHisVal 21
                                                                                                                                                                                                          /organism="Homo sapiens"
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/db xref="teaxon:9606"
/clone="CSODJO15YL11"
/tissue_type="T cells
10-normalized"
/plasmid="pCMVSPORT_6"
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60.03%
                                           (1-1505)
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Matches:
Conservative:
Mismatches:
Indels:
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1 (bases 1 to 1534)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
                                                                                                                                                                            Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                       Faraday Avenue
                                                                                                                                                                                                                                                                                                                                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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HTC; CNSLT_CDNA.
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                                                                                                                                                                  of Invitrogen
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/plasmid="pCMVSPORT_6"
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GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr 340
                                           ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu
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                                                                                 GGGGCCCTGGTCCGAGGCTTGAAGCGGGAGACTTGCGGCGGGGGCCTGGTCATGGTCAAG
                                                                                                  GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
                                                                                                                                       GTGACAGGCATTGAGATGTTCCACAAGAGCCTGGAGAGGCCGAGGCCGGAGATAACCTC
                                                                                                                                                          ValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnVal
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                           CCAGGTTCCATCAAGCCCCACCAGAAGGTGGAGGCCCAGGTTTACATCCTCAGCAAGGAG
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Pred. No.: Score: Percent Si Best Local Query Matc DB: US-10-039-	ORIGIN	FEATURES source	REFERENCE AUTHORS TITLE JOURNAL	ORGANISM REFERENCE AUTHORS TITLE	RESULT 11 AY105509 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	8 8 8 8 8 8
. No.: 1.48e-111		these are publicly available from ZmDB and may searching at MSL, maizemap.org; ZmDB, www.zmdb. www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. Wh maize cDNA sequences is either Virginia Walbot, Schnable, Iowa State, then clones may be requesewww.zmdb.iastate.edu. Location/Qualifiers 11193	2 (Dases 1 to 1193) 2 (Dases 1 to 1193) Coe,E.H. Direct Submitssion Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones,	M Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 1193) Hainey, C.F., Dolan, Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Overgo Probes	AY105509 AY105509 N Zea mays PCO100031 mRNA sequence. AY105509 AY105509.1 GI:21208587 HTC. Zea mays	
RESULT 12 CK215616/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM		Qy Db	Q B Q 8	F & B & B !	6	2 B & B & B & B
2 /c CK215616 1119 bp mRNA linear EST 09-DEC-2003 DN FGAS027583 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum cDNA, mRNA sequence. CK215616 CK215616.1 GI:39621720 EST. Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	720 CCTTTCTCCCTGGTTACCGCCCGCAGTTCTACAGTAGAGAACAAAATCATTAGG 953 720 CCTTTCTCCCTGGTTACCGCCCGCAGTTCTACAGGAACAACAAAATCATTAGGAAT	600 ATGCAGAAGGATGACATTGAGAGGCAGGCATGGTGCTGGCAAAGCCCGGCTCTATCACACCG 659 307 HisLysLysPheGluGlyGluIleTyrValLeuSerLysGluGluGlyGlyArgHisThr 326		GTGCCACAGCGGCAGACCGACCTCCCGTTCTTACTCGCTTGAAGATGTCTTCTCCATC AlaGlyArgGlyThrValValThrGlyArgIleGluArgGlyValValLysValGlyAsp	173 GJYSERALALEUNTGALALEUGUGUNALALYBALAGLYARMYAI	ATCACCGGCGCTGCGCANATGGACGGCGCCATCCTCGTCGTCGTCTCTGGCGCCGACGGTCCC MetProGlnThrArgGluHislleLeuLeuSerArgGlnValGlyValProHislleVal ATGCCGCAGACCAAAGAGCACATTCTCCTCGCCAAGCAGGTCGGCGTTCCCAAGATCGTT ValPheLeuAsnLysGlnAspMetValAspAspGlnGluLeuLeuGluLeuCalGluMet

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1 (bases 1 to 1119)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, I. Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, I. Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F. Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
Contact: Wm, L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the
phred (default parameters). It is the raw
identification of the high quality insert
(default parameters) has been run on this
the region [13,819].
Plate: L6B018 row: P. column: 19.
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University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
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    tIleThrGlyAlaAlaGlnMetAspGlyAlaIleLeuValValSerAlaAlaAspGlyPr 112
                                                GAACGGCCCCATAGGGGACACGTTGATTTTCCCCCGGTTACGCCGAATACTTCAAAAAACAT 1013
                                                                    GluAsnArgHisTyrAlaHisValAsp-CysProGlyHisAlaAspTyrValLysAsnMe
                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/clone = "Organ: Crown and leaf; Vector: pCMV SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20(S from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissu were
separature exposure. The last 6 populations: After 7 days
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissu were
separature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA)."
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1094.00
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Matches:
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CNS06YH3 960 bp DNA linear CSS 06-JUL-200 T3 end of clone AYOAAO09E08 of library AYOAA from strain CBS 6340 of Kluyveromyces thermotolerans, genomic survey sequence.
AL421021 AL421021.1 GI:12204218 GSS. Kluyveromyces thermotolerans
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipplytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
TEBS Lett. 487 (1), 3-12 (2000)
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/note="ent(<11...>958)
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/note="similar to Saccharomyces cerevisiae ORF YOR187w [
TUF1; translation elongation factor TU, mitochondrial]"
/evidence=not_experimental
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Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 899)

Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Widall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
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Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                   AlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProValGluAsp
                                                                                                                                                                                                                                                                                                                                                                           AlaAlaAspGlyProMetProGlnThrArgGluHisIleLeuLeuSerArgGlnValGly
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 AAGGTTGGAGAGACTGTTGACATTGTTGGATGAAGGATACAAGGAACGTCACAGTTACT
             LysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThrValThr
                                                             ValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGlyValVal
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/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
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| lab_host="DH10B"
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Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof01-lms1 row: g column: 03
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Fax: 814 865 9131
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Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
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CV291218.1 GI:52577294
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/note="Vector: pBluescript SK (+/-); Site_1: EcoRI;
Site_2: Xhol; This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"
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Search completed: April 24, Job time: 4496.89 secs

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-NO_MMAP -LARGEQUERY -NEG_SCORES0 -MARIT -DSPBIOCK=100 -LONGLOG
-DEU TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

	COMMENT		JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	BD082347
PI HAROLD KLEANTHOUS, LING LISSOLO, DEAN FRANCOIS TOMB, CHARLES FI MILLER, PI AMAL AL GARAWI PC A01N93/04, A01N59/16, A61K9/48, A61K31/70, A61K31/715, A61K39/02, PC A61K39/40, PC G01N33/554, G01N33/569	HUMAN GENOME SCIENCES INC PN JP 2001523954-A/54	WARCIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA.	corresponding polynucleotide molecules Patent: JP 2001523954-A 54 27-NOV-2001;	76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and	Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.	Viruses; dsDNA viruses, no RNA stage; Adenoviridae. 1 (bases 1 to 1448)	Mastadenovirus	JP 2001523954-A/54.	BD082347.1 GI:22627957	corresponding polynucleotide molecules. BD082347	76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and	BD082347 1448 bp DNA linear PAT 27-AUG-2002	

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ValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnVal
                                  ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr
                                                                                                                GTGGATGCCTATATCCCTACTCCAGAAAGAGACACTGAAAAAACTTTCTTGATGCCGGTT
                                                                                                                                                                         GluAlaLysAlaGlyAsnValGlyGluTrpGlyGluLysValLeuLysLeuMetAlaGlu
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/mol_type="genomic DNA"
/db_xref="taxon:10509"
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Nature 388
97394467
                    Direct Submission
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Medical Center Dr, Rockville,
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2 (bases 1 to 10532)

Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Fleischmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Fleischmann, R.D., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, E.F. Dougherty, B.A., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, E.F. Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.E., Gocayne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Bowman, C., Watthey, L., Wallin, E., Hayes, W.S., Borodovsky, M., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C.
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Helicobacter pylori 26695 section
Medical Center Dr, Rockville,
Location/Qualifiers
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Action		CDS	gene				CDS	gene						CDS	gene						CDS	gene						CDS	gene	
	כדי		/translation="MAKKVVGEIKLQIPAGKANPSPPVGPALGQRGVNIMEFCKAFNE RTKUMGSFNIPVIITYYQDKSFTFITKKPPVTDLIKKASGVEKGSDNPLKNKIAKLTH KQVEEIAQLKMEDLNTSTMBAAKKIVMGSARSMGVEVVD" Complement (2360 2880)	/product="ribosomat protein L11 (rp111)" /protein_id="AAD08248.1" /db_xref="GI:2314364"		3.83; identified		•	QVNFRVDKKGNVHAPIGKASFPEEKIKENMLELVKTINRLKPSSAKGKYIRNAALSLT MSPSYSLDAGELMDIK"	/ translation="MARKVPRKIEKLFSKIONDKAYGROVEVVKSLASAKFDETVE VALRIGVDFRHADDWGAVVLFHGTGKKVRVAKDIKODGAVKVAKAADVVGGDDLA FETYMGATIFFHGAVVLFHGTGKKVRVAKANGKOVFMATTAKAVAGADVVGGDDLA	/protein id="AAD08247.1" /db_xref="GI:2314363"	፫	/note="81mlar to GB:142023 SP:244342 F1::100316 PID:122450 PID:1204767 percent identity: 51.98; identified by sequence similarity; putative"	complement (11681872) /gene="HP1201"		NKARNOGIKVOVIKNTLÄHIÄMKETGYSDLDLKETNVFLWGGDQIALSKLVFDFQKEH KDHFYLKAGLFDKESVSVAHVEAVSKLPSKEELMGMLLSVWTAPARYFVTGLDNLRKA KFENL	/protein 1d="AAD08246.1" /db_xref="GI:2314362" /translari.n="MOKCHOBOHKVELVANT.KSOFADAKAKI.TCDVKGT.SVEKT.FAT.B	ein L10	30.38; identified by sequence similarity	to SP:P42923 PID:786163 GB:AL009126	/gene="HP1200" complement(5651059)	VNKEEAETIKKKLEEVGAKVEVK" complement (565. 1059)	/translation="MAISKEEVLEYIGSLSVLELSELVKMFEKKFGVSATPTVVAGAA VAGGAAAESEEKTEFNVILADSGAEKIKVIKVVREITGLGLKEAKDATEKTPHVLKEG	/protein_id="AAD08245.1" /db_xref="GI:2314361"	omal protein L7/L12	equence similarity,	to SP:P05392 percent identity:	•	/db xref="taxon:85962" complement(142519)	/organism="Helicobacter pylori 26695" /mol_type="genomic DNA" /strain="26695"
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                  GTGGTGAAAGTAGGCGATGAAGTGGAAATCGTTGGTATCAGACCTACACAAAAAACGACT
                                 ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr
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                                                                                                                                           ValAspAlaTyrIleProThrProGluArgAspThrGluLysThrPheLeuMetProVal
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/note="similar to
26.18; identified
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AL Patent: JP 2001502886-A 6 06-MAR-2001;
CHIRON BEHRING GMBH & CO
OS Helicobacter pylori
PN JP 2001502886-A/6
PD 06-MAR-2001
PF 25-JUL-1997 JP 1998508651
PR 26-JUL-1997 JP 1998508651
PR 26-JUL-1996 DE 196 30 390.7
PI BERNHARD KNAPP, ERIKA HUNDT, KARL HEINZ SCHMIDT PC
CI2N15/31,C07K14/205,C07K16/12,G01N33/53,A61K31/70,A61K39/106, PC
AALK39/395
CC Strandedness: Single;
CC Topology: Linear;
FH Key
1. 2825
FT source /organism='Helicobacter pylori'.
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BD009865.1 GI:186387
JP 2001502886-A/6.
Helicobacter pylori
Helicobacter pylori
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Knapp,B., Hundt,E. and Schmidt,K.H.
Proteins, in particular membrane proteins,
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preparation and use.
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                                                                                                                                                                               /organism='Helicobacter pylori'
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                                                                                                                                                                                                                                                                                                                                                                                                                                Street, Cambridge, MA 02139, USA
Address all correspondence to: hp@arcb.us.astra.com or Richard
A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge,
MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith,
Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills,
Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics
Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and
Diane E. Taylor are with the University of Alberta Department of
Medical Microbiology and Immunology, Edmonton, Alberta, Canada, T6G
2H7 and the Canadian Bacterial Diseases Network. All other authors
are with Astra Research Center Boston, 128 Sidney Street,
Cambridge, MA, 02139. Putative identifications, Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King, B.L., Alm, R.A. and Trust, T.J.
Direct Submission
Submitted (12-JAN-1999) Astra Research Center Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic-sequence comparison of two unrelated isolates of the gastric pathogen Helicobacter pylori
Nature 397 (6715), 176-180 (1999)
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Alm, R. A., Ling, L.S., Moir, D.T., King, B.L., Brown, E.D., Doig, P.C., Smith, D.R., Noonan, B., Guild, B.C., deJonge, B.L., Carmel, G., Tummino, P.J., Caruso, A., Uria-Nickelsen, M., Mills, D.M., Ives, C., Gibson, R., Merberg, D., Mills, S.D., Jiang, Q., Taylor, D.B., Vovis, G.F. and Trust, T.J.
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#Helticobacter pylori, strain J99
                                                                                                                                                                                                                                                                                                                                                                            alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web site. (URL: http://www.astra-boston.com/hpylori).
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Helicobacteraceae; Helicobacter.
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Helicobacter pylori J99
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                        complement (462.
                                                                        /product="50S RIBOSOMAL /protein id="AAD06710.1" /db_xref="GI:4155730"
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complement(257. .415)
                                                                                                                                                                                                                                                         complement (257. .415)
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                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                codon_start=1/transl_table=11
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                                                                                                                                                                 note="similar to H. pylori 26695 gene HP1204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:4155724
                                                                                                                                                                                                                                                                        xref="taxon:85963"
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section 102 of 132
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/gene="jhp1129"
2365. .4101
/gene="jhp1129"
/note="similar to F
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FVEVMSLTLLMPETITLASDBSRALDDKDWKMYYDFHHESSPVLMYFEFSFCLVGIYLF
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FMSFNAFLSLLTEITVIVFFYSTLILTNWKITLVFTTILALQIFFIVKKYTVLIKKKG
EMAAKSKAQTLKVFSKFFSNFKITKLKDNHEEAHKLFGENSRKAHDTEIIYSTLQVVF
RYSIETYGFSLLILAVAYILFFKYGEARWVLFTISMYALALYRILFSVTGVISYYNEIA
YNQLATNVVFKSLSKTIVEEDLVFULDENEKITLQNISFXYSKHFVLKNFNLTIQKGQ
KIALIGHSGCGKSTLADIIMGLTYPKSGEIFIUNTLLTSENRRSWRKKIGYIPQNIYL
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/note="synonym: jhp1131"
complement (4966. .5955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mAlevvlwDfDGvIfDSwHlKyEGFKAlfQKHGNDSKEGLKQFE
VYHYQSGGISRNEKIQYFYNEILKTFIAQEEIDALALEFGAIIEQKLfDRGHLNSEVM
AFIDKHYQNYIFHIASAALHSELQVLCEFLGITKYFKSVEGSPPDKPKIIANIIQKYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2365.
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GDNVGVLLRGTKKEEVERGMVLCKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="Wakektmethophunigtighvyhgkttelsaaisaulslikklaem
Koydnidna poekergitiatshi eyetetrhyahvdopghadyukmatigaagubga
Iluvsaandepmeqtrehillsroydhivyflukkomwiddellelelemeturelika
Yefpgddtpivagsalraleeakagnugewgekvikumaevdsyiptperdtektfelm
                           complement (6284.
                                                      NNEGLMSETEIKNILKKYGAYSLVTKTYMRFKADNKRAHKAVHTKECLHVLIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4966. .5955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="jhp1130"
complement(4110. .4778)
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/product="abc transporter,
/protein_id="AAD06712.1"
/db_xref="GI:4155732"
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                                                                                                                                                                                                                                                 'trans1 table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDPSRMLMIGDSVNDYESAKANKVAFLGYNSKVLKNLVGQDGYQGKYLESFKGFDLQN
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/note="similar to H. pylori 26695 gene HP1207"
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/note="similar to H. pylori 26695 gene HP1205"
                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                      note="similar to H. pylori 26695 gene HP1208"
                                                                                                                                                                                                                                                                                                                                                                                              gene="M.HpyI"
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/transl_table=11
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Best Local Similarity:
Query Match:
                                                                              Score:
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/reprojithmylnhdiendlqvsALNAASATIFLAHIAFIKSVSACRIARVDUREFILD
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/resastlnqssldfreefactvlnerkldllknqyfpefikslatssalserenvfkev
/resastlnqssldfreefactvlnerkldllknqyfpefikslatssalserenvfkev
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7507..7
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/note="synonym: jhp1133"
/note="synonym: jhp1133"
                                                                                                                                                                                   akkiseahsefsleeielslekvkkteirrmiiodkirpdkraleevrpisiesnilf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (8254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MKFLALFFLALAGVAFAHDGGMGGMDMIKSYSILGAMIGLGIAA
FGGAIGMGNAAAATITGTARNPGVGGKLLTTMFVAMAMIEAQVIYTLVFAIIAIYSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (7804. .8121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative"
/protein_id="AAD06716.1"
/db_xref="GI:4155736"
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| KRRFYFIARALSQLARFITGIEIHPGAKIGRGLFIDHGMGVVIGETTEIGDDVTIYHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ATP synthase F0, subunit
/protein_id="AAD06717.1"
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complement (7804. .8121)
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/gene="jhp1134"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to H. pylori 26695 gene HP1213"
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     Indels:
                             Mismatches:
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                                                                                                          ValValLysValGlyAspGluValGluIleValGlyIleArgProThrGlnLysThrThr
                                                                                                                                                                                                                                                           GluAepValPheSerIleAlaGlyArgGlyThrValValThrGlyArgIleGluArgGly
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                                                                                                                                                       GTAACCGGTGTAGAAATGTTTAGAAAAGAATTAGAAAAAGGTGAAGCCGGCGATAATGTG
                                                                                                                                                                          ValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnVal
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2 (bases 1 to 308929)
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Drescher,B. and Suerbaum,S.
Direct Submission
Submitted (27-MAY-2003) Institute of Hygiene and Submitted (27-MAY-2003) Josef Schneider Str. 2,
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Suerbaum, S., Josenhans, C., Sterzenbach, T., Drescher, B., Brandt, P.
Bell, M., Droge, M., Fartmann, B., Fischer, H.P., Ge, Z., Horster, A.,
Holland, R., Klein, K., Konig, J., Macko, L., Mendz, G.L., Nyakatura, Schauer, D.B., Shen, Z., Weber, J., Frosch, M. and Fox, J.G.
The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus
Helicobacter hepaticus
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7901-7906 (2003)
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Helicobacter hepaticus ATCC 51449
Bacteria, Proteobacteria, Epsilonproteobacteria,
Helicobacteraceae, Helicobacter.
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strain="ATCC 51449"
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PHSDLVALKYERHVCSGGSYDKINVSNLTIKKISEKPSNRDAYENVLMLGLTGYEISV
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MLDEESLYQIITQTKSSLLRQYQLLLDTEDIRLEFSDEAIRELARLSHNANQRTEDIG
ARRLHTTIERVLEDIGFDVDTYKGKEVEITGDMVRERLGDLVENIDLARYIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Locus_tag="HH0310"
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                                                                                 Score:
                                                                                                                Pred. No.:
                                          Percent Similarity:
                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (8218. .8757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /BC_number="2.4.2.18"
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016. .11430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="secA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="HH0317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="outer membrane lipoproteins carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_tag="HH0316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="lolA"
9.3e-116
1900.00
96.24%
91.73%
                                          Length:
Matches:
Conservative:
   Mismatches:
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IleThrLeuproGluGlyValGluMetValMetProGlyAsp 360
                                                                                                GlubeulleSerProValAlabeuGlubeuGlyThrLyaPhe 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nn="MADGLSEEEVKGVKIPLIYEKSTLMPAVNLQIVFTHAGSITDEI
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XEVEBEWKRGVIRAILVLVGGOVELEEVKKDLLSLLSVLPLGEEGE
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LGSEPLNETLSQRLSSAFSAYYRGLPDFAKEELHKIEALTLEEIN
ILSFSVVTAPKE
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n="WEPSDLLKLSKLHCKDALDFALLAPKGYEDRRPSSELVSGAEGV
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RRYQOERGIPKESTKVFKONGTLIELASRVLSKESLIAALGIPALYASRL
RRYQOERGIPKEHQEALKFAEIFRHLRALVGKKRSFEALCRCQNAPW
                                                                                                                                                                                                                                                                                                                                                                346792 bp DNA linear BCT 08-SEP-2003 es, complete genome; segment 2/7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eria; Epsilonproteobacteria; Campylobacterales;
Olinella.
                                                                                                                                                                                                      ArgThrValGlyAlaGlyValValSerAsnileIleGlu 399
||||||||||||||
AGAACAGTTGGTTCAGGTGTTGTAACAAAAATTATTGAG 55824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C., Eppinger, M., Raddatz, G., Simon, J.M., Nandakumar, R., Grose, R., Rosinus, A., . Linke, B., Meyer, F. and Lederer, H. ence and analysis of Wolinella succinogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03) Max-Plank Institut for Developmental
35, 72076 Tuebingen, GERMANY
alifiers
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="CAE09502.1"
T.34489502"
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VTATIVE PROCESSING PROTEASE"
|="CAE09501.1"
|I:34482501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolinella succinogenes"
genomic DNA"
MZ 1740"
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="WS0353"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "WS0352"
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LFVGVAYLINDLAFKLSLPILGILALYSVMKRFSFLAHLILGLSLALAPIAGVIAVSB
SVPLWSLFLSLGVLFWVAGFDVLYSLQDIEFDKNEGLHSIPSRFGEKKAILLSRIFHL
FTLFFWFLFVIFAPLGQIMLFAWAFCVMMLGYEHYLVSQDFRNIPKAFFTVNGYLGIV
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note="CONSERVED HYPOTHETICAL 19.7 KDA PROTEIN"
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16
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Matches:
Conservative:
                                                                                                                                                                                                                                                                   product="hypothetical protein"
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complement (9026. .935
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1862.00
94.96%
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                                                                                                            7353. .7838
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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PIEDVPSISGRGTVVTGRIBKGVVKVGDTIEIVGIKDTQTTTVTGVERFRKENDQGBA
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Parkhill, J., Wren, B.W., Mungall, K., Ketley, J.M., Churcher, C., Basham, D., Chillingworth, T., Davies, R.M., Feltwell, T., Holroyd, S., Jagels, K., Karlyshev, A., Moule, S., Pallen, M.J., Penn, C.W., Quail, M., Rajandream, M.A., Rutherford, K.M., VanVliet, A., Whichead, S. and Barrell, B.G. The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences
                                                                                                                                                                                                                                                                1660
                                                                                                                                    1661 ACTGATGTTACAGGTTCGATTAAATTAGCTGATGATGGTGTTGAAATGGCTATGCCAGGTGAA 1720
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Campylobacter jejuni subsp. jejuni NCTC 11168
Bacteria: Proteobacteria: Epsilomproteobacteria; Campylobacterales;
Campylobacteracese; Campylobacter.
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RL, http://www.sanger.ac.uk/Projects/C_jejuni/).

Location/Qualifiers

1. .308601

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/db_xrafe="texon:19222"

complement(101..886)

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GlyValLeuLeuArgGlyThrLyBLy8GluGluValGluArgGlyMetValLeuCy8Ly8
                                   1481 GGTGTTCTTCTTCGTGGTACTAAAAAAGAAGAAGTTATCCGTGGTATGGTTACCTAAA
                                                                                                         ProGlySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu
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NCTC 11168 complete genome;
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Submitted (09-FEB-2000) Submitted on behalf of the Campylc
sequencing team, Sanger Centre, Wellcome Trust Genome Camp
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
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Campylobacter jejuni subsp. jejuni
segment 2/6
AL139075 AL11168
AL139075.2 GI:6967817
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CDS

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chain, len: 392 as, highly similar to many e.g. TRPB THEMA
tryptophan synthase beta chain (EC 4.2.1.20) (389 as),
fasta scores; opt: 1476 z-score: 2082.2 E(): 0, 59.9%
                                                                                                                                                                                                                                                                                                                                                                                             FKRAFHSEIIGSSAYDNAKDIKDILSGRMQGAKFDLVVLNAMFALYTANKASSPLVAK
DMILEAIYSGKVIEYPKEYQAYAKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00117 GATase, Glutamine amidotransferases class-1, score 252.00, E-value 8.4e-72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="PS00442 Glutamine amidotransferases class-I active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /noce="Cj0347, trpF, probable
N-(5'-phosphoribosyl)anthranilate isomerase, len: 199 aa;
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N-(5'phosphoribosyl)antranilate (PRA) isomerase, score
102.30, E-value 9.5e-27"
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gene="trpB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Cj0345; ripp, possible anthranilate synthase component 1, len: 416 aa; similar in C-terminal half to many e.g. TRPE_CLOTM anthranilate synthase component I (EC 4.13.27) (494 aa), fasta scores; opt: 784 z-scores: 1209.9 E(): 0, 47.0% identity in 281 aa overlap. 35.6% identity in 365 aa overlap to HP1282. Contains Pfam match to entry PF00425 chorismate bind, chorismate binding enzyme, score 309:50, E-value 3.9e-89"
/codon start=1
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                                                                                                                                            /translation="METTDLPYLIGIISGIASGLFGIGGGMIIVPSMFALGASAHHA
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PILAYFLGYDSKKVVSLSLFFFVIFASVSGIISFSNSGVIDSBVIHKGILVGIASMVGV
FIGIKIIEKOHISAHRKILLCVYALSILGTHSLINKLINFINF
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FSEFKAKYYEALSKNXICDFAGFFGVFSANFVSLFEKIPLSSKKNYDFPLFLFANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLIYEKNSKMFFKFGASKYFBYLKDDIEPMKKKQKNDFEILNSLEDEKNDFLKMCEKA
KEYLLSGDIPQVVLSKQLCIKHQVNAPDYYESLSALNPSAYMFYFPSKYGVVLGSSPE
FLLKIKKREIYLAPIAGTRNLENNCDLLALEKDLLSDEKELSEHKMLVDLARNDASKF
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chorismate binding enzyme, score 309.50, E-value 3.9e-89"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative anthranilate synthase component I"
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                          product="putative integral membrane protein"
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db_xref="GI:6967818"
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                                                                                                                        _xref="UniProt/TrEMBL:Q9PIF7"
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/gene="trpE"
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/gene="trpD"
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ACTGATGTTACAGGTTCGATTAAATTAGCTGATGTGTTGAAATGGTTATGCCAGGTGAA 121388
                                                     GGTGTTCTTCTTCGTGGTACTAAAAAGAAGAAGTTATCCGTGGTATGGTTCTTGCTAAA 121208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other sequences; artificial sequences.

1 (bases 1 to 1185)
Gaucher, E.A., Thomson, J.M., Burgan, M.F. and Benner, S.A.
Gaucher, E.A., Thomson, J.M., Burgan, M.F. and Benner, S.A.
Inferring the palaceonvironment of ancient bacteria on the basis of resurrected proteins
Nature 425 (6955), 285-288 (2003)
                                                                                                                                                                                                           ThraspValThrGlySerIleThrLeuProGluGlyValGluMetValMetProGlyAsp 360
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Gaucher, E.A., Thomson, J.M., Burgan, M.F. and Benner, S.A.
Direct Submission
Submitted (22-MAX-2003) Chemistry, NASA Astrobiology Institute,
Box 117200, Gainesville, FL 32611-7200, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   AlaileArgGluGlyGlyArgThrValGlyAlaGlyValValSerAsnIleIleGlu 399
                                                                                    ProglySerIleThrProHisLysLysPheGluGlyGluIleTyrValLeuSerLysGlu
                                                                                                    GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr
                                                                                                                                                                 GAAGGIGGTAGACATACTCCATICTTTAACAACTATAGACCACAGTTTTATGTAAGAACA
                      GlyValLeuLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys
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1. .1185
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TITLE
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AUTHORS
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identity in 384 as overlap. 56.4% identity to HP1278. Constains PS00168 Tryptophan synthase beta chain pyridoxal-phosphate attachment site, PS00017 ATP/GTP-binding site motif A (P-loop), and Pfam match to entry PF00247 trp_syntB, Tryptophan synthases, beta chain, score 806.40, B-Value le-238" /codon_start=1
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36
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Conservative:
Mismatches:
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93.23%
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AY305397.1 GI:32186881
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Inferring the palaeoenvironment of ancient bacteria on the basis resurrected proteins
Nature 425 (6955), 285-288 (2003)
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USA
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Gaucher, E.A., Thomson, J.M., Burgan, M.F. and Benner, S.A.
Direct Submission
Submitted (22-MAY-2003) Chemistry, NASA Astrobiology In
Box 117200, Gainesville, FL 32611-7200, USA
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ancestral elongation factor Tu
           2 (bases 1 to 1185)
Gaucher, E.A., Thomson, J.M., Burgan, M.F. and Benner, S.A.
Direct Submission
Submitted (22-MAY-2003) Chemistry, NASA Astrobiology Institute,
Box 117200, Gainesville, FL 32611-7200, USA
Location/Qualifiers
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rAcGACTTTCCAGGTGATGACGTGGCGGTTATTCGTGGTTCTGCGCTGAAAGCACTGGAA
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                                                                                                                                  LeuLeuSerArgGlnValGlyValProHisIleValValPheLeuAsnLysGlnAspMet
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ATGGCGAAAGAAAAGTTTGAACGTACAAAACCGCACGTGAACATTGGTACTATCGGCCAC
                     ValAspHisGlyLysThrThrLeuSerAlaAlaIleSerAlaValLeuSerLeuLysGly
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Weissenbach, J. and Boucher, C.A.

Nature 115 (6871), 497-502 (2002)
                                                                                                                                                 Betaproteobacteria; Burkholderiales;
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Location/Qualifiers
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                                                                                                                    Ralstonia solanacearum
Bacteria, Proteobacteria,
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AL646073.1 GI:17429991
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Boucher, C.A.
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="structural elements; cell exterior; surface
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Gene name confidence ; probable
predicted by Codon_usage
predicted by FrameD"
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37
47
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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complement (2401. .2973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function="structural elements; cell exterior; surface
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biosynthesis; chorismate; probable
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Gene_name_confidence: probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Product confidence : probable Gene name confidence : probable predicted by Codon_usage predicted by Homology predicted by FrameD"
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transl_table=11
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predicted by Homology
predicted by FrameD"
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gene

CDS

gene

CDS

9

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                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae: Caulobacter.

[ Jases I to 793, M. C. Reldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Poccka, I.Y., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Haft, D.H., Kolonay, J.F., Durkin, A.S., Gwinn, M.L., Shetty, J., Barry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGVLLRGTKREDVERGOVLCKPGSITPHTKFVAEAYILTKEEGGRHTPFFTNYRPQFY
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Nierman, W.C., Feldbiyum, T.V., Paulsen, I.T., Nelson, K.E., Bisen, J.,
Heidelberg, J.F., Alley, M.R.K., Obta, N., Maddock, J.R., Potocka, I.,
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Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L.,
Baft, D.H., Kolonay, J.F., Smit, J.J., Caven, M., Khouri, H., Shetty, J.,
Berry, K., Utterback, T., Tran, K., Wolf, A., Vanathevan, J.,
Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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Submitted (31-3AN-2001) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-Tu
                                                                                                                                                                                                                                                                               Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
21173698
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Caulobacter crescentus CB15
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AE005800.1
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                                                                       ORGANISM
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PUBMED
REFERENCE
AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FACGWTVTLLERLVDASAEDFGLRTATLRAGGRVVAAELGLLSEGRYHLWLPIYDPEF
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RPMRVMGAARLARRFDRIVACEPGLVGQLRGGGGGFLATLARRYPRLGAALGLGFGLVG
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                                                      complement (142. .1332)
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transI table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
                                                                                                                                                                          GlyValLeuLeuArgGlyThrLysLysGluGluValGluArgGlyMetValLeuCysLys 300
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                                                                                                                                                                                                                                                                                                                                                                                                              GluGlyGlyArgHisThrProPhePheThrAsnTyrArgProGlnPheTyrValArgThr 340
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Submitted (31-2MN-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaileArgGluGlyGlyArgThrValGlyAlaGlyValValSerAmileIleGlu 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus CB15
Caulobacter crescentus CB15
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                           GGCGTGCTGCTGCGCGGCACCAAGCGTGAAGACGTCGAGCGCGGCCCAGGTGCTGTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnValLys1leThrValGluLeuIleSerProValAlaLeuGluLeuGlyThrLysPhe
                                                      261 ValThrGlyValGluMetPheArgLysGluLeuGluLysGlyGluAlaGlyAspAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
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AE005984.1 GI:13424876
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TATPASPLPFTVRAPVRPAPAGTPSLEVPASALARPGVAI RPAPLPGDSAGDLRTALR
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Matches:
Conservative:
Mismatches:
Indels:
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EST526371 EST526597

CD812340 CD8142340 CD814221 CD819111 CC239056 ACC27970 CC027685 CC027685 CC027685 CC027685 CC027685 CC027685 CC02438 BEC02438 BFC02438 BFC02438 BFC02438 BFC02438 BFC02438 BFC02438 ACC2768001 CC0514609

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Run on:

Seguence:

Searched:

Database

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (Dases 1 to 958)

Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warter,W., Garves,T., Mardis,E. and Wilson,R.
Gallus gallus BaC End Reads
Unpublished (2003)
Contearc: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watcson.wustl.edu
Insert Length: 182000 Scd Error: 0.00
Seg primer: Sp6 ATTAGGTGACTATAGG
Class: BAC ends
High quality sequence start: 7
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23.6; DB 8;
Pred. No. 1.9e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .958
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db xref="taxon:9031"
/clone="CH261-90B21"
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BES59176
BF88025
CD812420
CD812420
CCB15821
CCC31905
CCC31905
CCC217034
BIZ08331
BIZ
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CC266736.1 GI:30616030
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Gallus gallus
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Best Local Similarity 86.7%;
Matches 26; Conservative C
                                             489
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231
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422
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510
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DEFINITION
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BH612485 SALK 0328
AG394257 Mus muscu
AG088415 Pan trog1
BX207173 Danio rer
AL381307 MtEC019B1
CR355923 Medicago
AL457517 T. brucei
AL457517 T. brucei
AL457517 T. brucei
AL457517 T. brucei
BR431207 BGGSWISTF
BZ503289 BONGESERT
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ZMMBBb055
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HV_CED002
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                                                                                                                                           April 24, 2005, 00:31:54 , Search time 1642.13 Seconds (without alignments) 718.576 Million cell updates/sec
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CL010460
AL977636
AZ161299
CO578276
CF114243
AZ138814
BF065214
                                                                                                                                                                                                                                                                                                                                                                                                                     68479088
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  nucleic search, using sw model
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AL381307
AL381308
CR325923
TA68E10P
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Maximum DB
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Gaps

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Length 958; Indels

Regult è.

DEFINITION

AA516958

RESULT

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ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Discussion to 751)

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submitsed

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-15-503-9170)

Clones are derived from the mouse BAC library MSNg01. For BAC
library availability, please contect Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG394257 151 bp DNA linear GSS 03-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-213C16.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="SAIX 03286"
/clone="AAIX 03286"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Squence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At3904770. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 418)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 418;
                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA FEAX: 858 558 658 678 578 Eax: 858 558 678 678 Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .418
/organism="Arabidopsis thaliana"
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Pred. No. 4.3e+02;
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BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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GSS.
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Mus musculus molossinus
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TITLE
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AG394257
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                                                                                                                                                                                 TITLE
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BH612485.1 GI:18060449
GSS.
                                                                                                                                                                              AA516958 550 bp mRNA linear EST 14-JUL-1997 vh85d10.rl Knowles Solter mouse E6 5d whole embryo Mus musculus cDNA clone IMAGE:893779 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 550)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Knowles Solter mouse E6 5d whole embryo" /note="Vector: pBluescribe (modified); Site 1: Mlu1; Site 2: Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: Sal1(dT): 5'-CGGTCGACCGTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev stage="embryo (post-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/errain="c57BL/6J x DBA/2J Fl"
/dD_xref="taxon:10090"
/clone="1MAGE:893779"
     925 GCTTATATTTAATAATATTTGGTCCCAA 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 352.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                             AA516958.1 GI:2256417
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                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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FEATURES

DEFINITION

RESULT 3 BH612485

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Contact: Genoscope
                                    Query Match
Best Local Similarity
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.

Submitted (12-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchitro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:sla 145-503-9111, Fax:sla 45-503-9117)
Tel:sla 145-503-9111, Fax:sla 45-503-9110,
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG088415 1092 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-087F20.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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BAC end sequences of Library PTB
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71.6%; Score 22.2; DB 9; Length 751;
Best Local Similarity 88.9%; Pred. No. 6e+02;
Matches 24; Conservative 0; Mismatches 3; Indels
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                 /sex="male" /
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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/mol_type="genomic DNA"
/sub_sepecies="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-213C16.TJ"
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-087F20.F"
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                                                                                                                                                                  Location/Qualifiers
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Pan troglodytes
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                                                                         Sequencing : TJ
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R.Site 2
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                                                                                                            Vector
R.Site 1
R.Site 2
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Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 234E10. 234E10
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL381307 416 bp mRNA linear EST 03-AUG-2000 MtBC019B10F1 MtBC Medicago truncatula cDNA clone MtBC019B1 T3, mRNA Bequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledona, core eudicots;
rosida, eurosida I; Fabales, Fabaceae, Papillonoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from endomycorrhizal roots
                                                                                                                                                                                                                                                       BX207173 589 bp DNA linear GSS 29-JAN-
Danio rerio genomic clone DKEY-234E10, genomic survey sequence.
BX207173
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     Length 1092;
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Location/Qualiflers
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Pred. No. 8.4e+02;
0; Mismatches 2;
  Score 22; DB 9; I
Pred. No. 7.1e+02;
0; Mismatches 5.
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Humphray, S.J., Huckle, B. and Durham, J.L.
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/organlsm="Danio rerio"
/mol_type="genomic DNA"
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/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                  297 CTAATATAAATAAAATTTCTCACTAC 326
                                                                                                        2 CTAATATTCAATAATATTGCTCACAAC 31
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71.0%;
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Best Local Similarity 92.0
Matches 23; Conservative
                                                    25; Conservative
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Best Local Similarity
Matches 24; Conserv
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// clone lib="wtbC"

// clone lib="wtbC"

// note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
Xho1; wh. truncatula sterilised seeds were germinated for
72h at 25 C, Defore transplanting into a 1/3 Epoisses soil
1: 2/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuecular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate
LPA8). The plants were watered every day and twice a week
with a modified nutrient Long Ashton solution without
phosphate but with a high level of nitrate. After 3 weeks
RNA was extracted from whole root systems. CDNA was
prepared from polyA+ enriched RNA. The CDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France). Note: EST may be of
fungal origin."
                                                                                                                                                                                                                                                                                                                                                                            /clone="MtBC019B1"
Lissue_type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus
intraradices"
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rogids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.coulouse.inra.fr/Mtruncatula.html).
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chategnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                      'organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Jemalong"
/db_xref="taxon:3880"
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AL381308.1 GI:9681059
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il Similarity 85.7%;
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/dev_stage="harvested 3 weeks post inoculation with Glomus
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Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31336 Castanet-Tolosan Cedex, France (Email : Mt-est@toulose.inra.fr Website :
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                                                                                                                                                                                                     http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
                                                                                                                                                                                                                                                                                                                                                       organism="Medicago truncatula"
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Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC019B1"
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RESULT 10 TA68E10P/c

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT

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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 580)
S Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                             "Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
thall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
thillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                Trypanosoma brucei
Trypanosoma brucei
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae;
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Pred. No. 9.9e+02;
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/organism="Trypanosoma brucei"
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85.7%; Pred. No. 5...
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/strain="TREU927"
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/clone="68f10"
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Matches 24; Conserv
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AQ491708
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED9274 GUTA 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell: Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.asnger.ac.uk/Projects/T_brucei/.
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/note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI ; Debelle F. and Chalhoub B.~Genoscope sequence ID : mtel-53124RM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                Gape
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1 (bases 1 to 557)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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T. brucel sheared genomic DNA clone 68f10, forward sequence,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
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clone="68e10"
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Matches 24; Conservative
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Matches 24; Conserve
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ORIGIN

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS

TA68F10P/c

RESULT 11

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Gaps

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GSS 24-APR-1999

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Query Match 69.7%;
Best Local Similarity 85.7%;
Matches 24; Conservative (
                                                                                                                                                             Brassica oleracea
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BOGSW15TF BOGS Brassica oleracea genomic clone BOGSW15, genomic
Burvey sequence.
BH433207
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Brassica oleracea
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
I (bases I to 70)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOGSW15TR
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
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RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                           Gaps
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genomic DNA inserted into PHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: FF
Class: sheared ends.
Location/Qualifiers
1. 720
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Pred. No. 1e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica oleracea"
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                                               Location/Qualifiers
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/db_xref="exaon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 TAATATTCTTCCATTATATAGCTCACAA 291
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1 Similarity 85.7%;
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Matches 24; Conserv
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BZS03289 782 bp DNA linear GSS 16-DEC-2002
BONGE68TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONGE68,
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PUFGO46TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa314H19,
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Wararyota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; euroside II; Brassicales; Brassicaceae; Brassica.
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1 (bases 1 to 832)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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/db xref="taxon:3712"
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/clone lib="BO_1.6 2 KB tot"
/clone lib="BO_1.5 3 ite 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHÖS1 using BstXI linkers"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Other GSSs: BONGE68TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
Fax: 301-388-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 782;
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TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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Pred. No. 1e+03;
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/organism="Brassica oleracea"
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Unpublished (2003)
Other_GSSs: PUFGO46TD
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                                              genomic survey sequence.
BZS03289
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                                                                                                          BZ503289.1 GI:27021620
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: Tr
Class: sheared ends.
Location/Qualifiers
Location/Qualifiers
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Search completed: April 24, 2005, 05:28:25 Job time: 1643.13 secs

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Staphyloc Staphyloc Staphyloc Homo Bapi Zebrafish

Zebrafish Zebrafish

Zebrafish

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Minimum DB Maximum DB

Database

Searched:

Homo Ношо

Mus muscu

Ношо варі

nucleic

Run on:

Sequence:

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SM mastadenovirus
Viruses; dabNA viruses, no RNA stage; Adenoviridae.

Viruses; dabNA viruses, no RNA stage; Adenoviridae.

Xicanthous, H., Lissolo, L.; Tomb, J.F., Miller, C. and Garawi, A.A.

76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polymucleotide molecules
corresponding polymucleotide molecules
HORANAX SOCIETE EN NOW COLLECTIF PASTEUR MERIEUX SERUMS ET
WACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC
PN JP 2001523954-A/60
PD 27-NOV-2001
PF 31-MAR-1998 JP 1998541962
PF 31-MAR-1998 JP 1998541962
PF 31-MAR-1998 JP 1998541962
                                                                                                                                                                                                                                                                                                                                                     BD082353 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
                                      AC134998 Homo Bapi
AC132329 Mus muscu
AC046177 Homo Bapi
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A01N43/04,A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
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                                                                                          AP004823
AP003359
AP003359
AP003359
BX089559
BX08559
BX065126
BX567304
AC138921
BX957304
AC138828
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AC138808
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AC134998
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AC046177
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AC107303
BX897661
BX088559
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AP004823
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G01N33/S54,G01N33/569
Strandedness: Single,
Topology: Linear;
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JP 2001523954-A/60.
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AC102439 Mus muscu
AC107741 Mus muscu
AC107741 Drosophil
AC009741 Drosophil
AE003695 Drosophil
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BD082355 76 kDa, 3
BD082347 76 kDa, 3
BD009865 Proteins,
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Antigenic
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AE001541 Helicobac
BD061867 Antigenic
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                                                                      April 23, 2005, 17:27:10 ; Search time 804.69 Seconds (without alignments) 1866.696 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                       gctaatattattcaataatattgctcacaac 31
                                                                                                                                                                                          4708233 segs, 24227607955 residues
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                   nucleic search, using sw model
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94.8 968
94.8 184688
74.8 212995
73.5 122995
73.5 122995
73.5 122995
73.9 26863
72.9 110000
72.9 269050
71.6 175477
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100.0%; Score 31; DB 6; Length 31; 100.0%; Pred. No. 3.6; cive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 31; Conservative

AL935255 Lactobaci AL954814 Zebrafish CR376780 Danio rer CR293523 Danio rer

AL954814 CR376780

Result š. CR293523

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AUTHORS Knapp, B., Hundt, E. and Schmidt, K.H.
TITLE their preparation and use TOURNAL Proteins, in particular membrane proteins, of Helicobacter pylori, their preparation and use TOURNAL Patent: JP 2001502886-A 6 06-MAR-2001;

ENT DS Helicobacter pylori
PN JP 2001502886-A 6
PD 06-MAR-2001
PR 25-JUL-1997 JP 1-7
PR 25-JUL-1997 JP 1-7
PR 26-JUL-1-7
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PP 25-JUL-1997 JP 1998508651

PR 26-JUL-1996 DE 195 30 390.7

PI BERNHARD KNAPP, ERIKA HUNDT, KARL HEINZ SCHMIDT PC
C12N19/395

CC Strandedness: Single;
CC Strandedness: Single;
CC Topology: Linear;
FH Key

FT source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP 2001502886-A/6.
Helicobacter pylori
Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD009865 2825 bp DNA linear PAT 31-JAN-200 Proteins, in particular membrane proteins, of Helicobacter pylori,
                                                        A01N43/04, A01N59/16, A61X9/48, A61X31/70, A61X31/715, A61X39/02, A61X39/40, A61X39/40, A61X33/40, A61X33/569
Strandedness: Single, Topology: Linear;
31-MAR-1998 JP 1998541962
HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/organism='Helicobacter pylori'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 6; Length 2825; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                 Length 1448;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                          Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                   Score 31; DB 6;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                         1324 GCTAATATTCAATAATATTGCTCACAAC 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2097 GCTAATATTATTCAATAATATTGCTCACAAC 2067
                                                                                                                                                                                                                                                                                                                                                                     1 GCTAATATTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCTAATATTCAATAATATTGCTCACAAC 31
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                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                           1. .1448
/organism="Mastadenovirus"
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                                                                                                                                                                                                                                /mol_type="genomic DNA'
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                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                Local Similarity 100.
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Matches 31; Conserv
                                                      ECC SSSE
                                                                                                                                                                                                                                                                                                     Query Match
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BD009865/c
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                  Mastadenovirus
Viruses; dabnA viruses, no RNA stage; Adenoviridae.
Viruses; dabnA viruses, no RNA stage; Adenoviridae.

E 1 (bases 1 to 31)
S Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
76 Kba, 32 kba, and 50 kba helicobacter polypeptides and
corresponding polynucleocide molecules
RABIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCIUS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC
PN JP 2001223954-A/62
PP 31-MAR-1998 JP 1998541962
PP 31-MAR-1998 JP 1998541962
PI HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES PI
                                                                                                                          BD082355
76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polynucleotide molecules.
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Mastadenovirus
Viruses; daDNA viruses, no RNA stage; Adenoviridae.
Viruses; daDNA viruses, no RNA stage; Adenoviridae.

1 (bases 1 to 1448)
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
corresponding polynucleotide molecules
Patent: JP 2001523954-A 54 27-NOV-2001;
MRENEUX OSCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCING SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES, INC
                                                                                                                                                                                                                                                                                                                                                                          ΕÏ
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A01013/04,A010159/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
A01013/30,A010133/569
Strandedness: Single;
Strandedness: Linear,
Foplogy: Linear,
Key
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76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
BD082347
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       31
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                                      GCTAATATTTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 31; DB Similarity 100.0%; Pred. No. 3.6 31; Conservative 0; Mismatches

    .31
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JP 2001523954-A/54.
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27-NOV-2001
                                                                                                                                                                                               BD082355.1 GI:22627965
JP 2001523954-A/62.
                                                                                                                                                                                                                                   Mastadenovirus
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Best Local Similarity
Matches 31; Conserv
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PI AMP
PC AO
PC AC
PC G
CC G
CC C
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BD082347/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                               LOCUS
                                                                                                                                                                                                                                                      ORGANISM
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TITLE
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TITLE
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KEYWORDS
SOURCE
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                                                                                                             BD082355
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QVNFRYDKKGNVHAFGKASFPEEKIKENMLELVKTINRLKFSSAKGKYIRNAALSLT
MSPSYSLDAQELMDIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transT_table=11
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complement (2360. .2899)
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/producE=transcription termination factor NusG (nusG)"
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                                                                                                         / LTÄNS JATION="MOKOHOROHKVELVANLKSOFADAKALLI CDYKGLSVRKLEALR
NKARNOGIKVOVIKNTLAHIAMKETGYSDLDLKETNVFLWGGDQIALSKLVFDFOKEH
KDHFVLKAGLFDKESVSVAHVEAVSKLPSKEELMGMLLSVWTAPARYFVTGLDNLRKA
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GB:U00096 PID:1790414 percent identity: 41.04; identified
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="similar to SP: P23375 percent identity: 55.10; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SP:P29395 GB:Z11839 PID:48184 GB:AE000512 percent identity: 63.83; identified by sequence similarity; putative" (coden start=1 /trans1 table=11
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db_xref="G1:2314362"
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complement (3354. .3512)
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complement(1917..2342)
/gene="HP1202"
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complement(1168. .1872)
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transl_table=11
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/transl_table=
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SM Helicobacter pylori 26695

Bacteria, Profesbacteria, Epsilonproteobacteria, Campylobacterales, Helicobacteracae, Helicobacter.

El (bases 1 to 10532)

S Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A., Sutton,G.G., Fleischmann,R.D., Ketchum,K.A., Klenk,H.P., Gill,S., Kirkness,E.F., Dougherty,B.A., Nason,K., Quackenbush,J., Zhou,L., Kirkness,E.F., Glodek,A., McKenney,K., Fitzegerald,L.M., Lee,N., Adams,M.D., Hickey,E.K., Berg,D.E., Goograe,J.D., Utterback,T.R., Peterson,J.D., Kelley,J.M., Karp,P.D., Smith,H.O., Fraser,C.M. and Venter,J.C.
                                                                      AE000626 10532 bp DNA linear BCT 06-APR-1999
Helicobacter pylori 26695 section 104 of 134 of the complete
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vaggaaasseekteenviladsgaekikvikvvreitglglkeakdatektphvlkeg
vnkeeaetikkkleevgakvevk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There is to 10532)

2. (bases I to 10532)

Fleischmann, R.D., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Fleischmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Kirkness, B.F., Bougherty, B.A., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, B.F., Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzgerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.B., Gocayne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 10532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-MAR-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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/protein id="AAD08245.1"
db_xref="GI:2314361"
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codon start=1

(rrans] table=11
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/ Organism="Helicobacter pylori 26695"
/mol type="genomic DNA"
/strain="26695"
/db.xref="taxon:85962"
complement (142. .519)
/gene="HP1199"
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/gene="HP1200"
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/transl_table=11
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AE000626.1 GI:2314360
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       RESULT 5
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gene **trna** gene **tRNA**

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Direct Cambridge, MA 02139, USA Research Center Boston, 128 Sidney Street, Cambridge, MA 02139, USA Address all correspondence to: hp@arcb.us.astra.com or Richard A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and Diane B. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta Canada, TGG 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative identifications, sequence alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web Site. (URL)
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PUNDVELIAGRGTVVTGRIERGYVKYGDEVELVGIRATOKTTVTGVEMERKELERGER
PUNGVLLRGTKKEEVERGWVLCKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRP
QFVVRTIDVTGSITLPEGVEWVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAG
VSNIIE"
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kdydnidnapoekergitlatshieyetetrhyahvdcpghadyvknmitgaaqmdga
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                       Helicobacter pylori J99
Helicobacter pylori J99
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                              1 [bases 1 to 1529)
Alm R.A., Ling, L.S., Moir, D.T., King, B.L., Brown, E.D., Doig, P.C., Smith, D.R., Ling, L.S., Moir, D.T., King, B.L., Garmel, G., Turnen, D. J., Caruso, A., Uria-Nickelsen, M., Mills, D.M., Ives, C., Gibson, R., Merberg, D., Mills, S.D., Jiang, Q., Taylor, D.E., Vovis, G.F. and Truet, T.J. Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
Nature 337 (6715), 176-180 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="similar to H. pylori 26695 gene HP1204"
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| transl_table=11
| producic="ELONGATION FACTOR TU (EF-TU)"
| protein id="AAD06711.1"
| db_xref="G1:4155731"
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transI table=11
product="50S RIBOSOMAL PROTEIN L33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Helicobacter pylori J99"
/mol type="genomic DNA"
/strain="J99"
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Location/Qualifiers
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King, B.L., Alm, R.A. and Trust, T.J.
Direct Submission
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complement(257. .415)
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db_xref="GI:4155730"
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complement(462. .1661)
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complement(257, .415)
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                                                                                                                                                                                                                                                                                                                                       /tränslation="makekfnrtkphynigtighydhgkttlsaaisavlslkglaem
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illvysaadgpmpqtrehillsrqygyphiyvflnkQdmyddgellelyemeyrellsa
                                                                                                                                                                                                                                                                                                                                                                                                                        YEFPGDDTPIVAGSALRALEEAKAGNVGEWGEKVLKLAMAEVDAYIPTPERDTEKTFLM
PYEDVPSIAGRGTVYTGRIERGYVKVGDEVEIVGIRPTQXTYTGYDEMFRELEKGEA
GDNVGVLLRGTKKEEVERGMVLCKPGSITPHKKFEGEIYVLSKEEGGRHTPFFTNYRP
OFYVRTTDVTGSITLPEGVEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAG
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Helicobacter pylori, strain J99 section 102 of 132 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SP:P22638 PID:142020 percent identity:
26.18; identified by sequence similarity; putative"
/codon starta
                                                                                                                                         /note="similar to SP:P42482 PID:587590 percent identity:
89.50; identified by sequence similarity; putative"
                                                                                                                                                                                              /codon_start=1

transl_table=11

/product="transl-ton elongation factor EF-Tu (tufB)"

/protein_id="AAD08250.1"

/db_xref="GI:2314366"
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'protein_id="AAD08251.1"
'db_xref="GI:2314367"
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complement (5186. .5258)
/gene="tRNA-Thr-2"
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complement (4982. .5055)
//gene="tRNA-G1y-2"
complement (4982. .5055)
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complement(5074. 5155)
/gene="tRNA-Tyr-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4877. .4948)
/gene="tRNA-Thr-1"
complement (4877. .4948)
/gene="tRNA-Thr-1"
/product="tRNA-Thr1"
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/prodnrt-"----
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/gene="tRNA-Tyr-1"
/product="tRNA-Tyr"
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/gene="tRNA-Thr-2"
                             complement (3548. .4747)
                                                                                   complement (3548. .4747)
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/trans1_table=11
                                                                                                                 'gene="HP1205"
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AE001541 AE001439
AE001541.1 GI:4155724
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Best Local Similarity 100.
Matches 31; Conservative
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/trānslation="mldlsyslerylogedpaarnkwevlllypgihallcyrlahalh
Krrfyfiarlisglarfitgibihpgakigrclfidhgwyygettbigddytyyg
VTLGGTGKFKGKRHPTLGNRVVVGAGAKVLGAICVGDDVRIGANAVVLSDLPTGSTAV
GAKAKTITKDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                968 bp DNA linear PAT 27-AUG-2002 composition and method of detection for Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAD06718.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRYPTQITLMVLNHDIENDLQVSALNAASATLFLAHIAPIKSVSACRIARVDNEFIIN
SASILNQSSLDLFVSGTRSELNMIERRSLGQVALAEBFLAHEALERAGKSLKETCA
LYEEAFTPYQNELLFREGEGIVENNERLLDLKNQYPDEIIKGIESSALSERERVPKEY
AKKISBAHSBESLEEIELSLEKVKKTEIRRMIIQDKIRPDKRALEBVRPISIESNLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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1 (bases 1 to 968)

Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.
Antigenic composition and method of detection for Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product = "POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE"
                                                                                                                                                                                                                                                                 note="similar to H. pylori 26695 gene HP1211"

/codon start=1

/transl table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 15292; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="8ynonym: jhp1135"
complement (7804. .8121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym: jhp1136"
complement(8254. .10320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (8254. .10320)
                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (7804. .8121)
                                        db xref="GI:4155735"
                                                                                                                                                                   7507. .7602
/gene="jhp1134"
7507. .7602
/gene="jhp1134"
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/transl_table=
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JP 2001517091-A/201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="atpE"
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synthetic construct
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BD061867
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Best Local S
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BD061867/c
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DEFINITION
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                        /Crainblation="MAKKGHKIPTLKYPLRSLKQIYRLJTFKEKMIFFLLVLMAVFSS
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RMFYGVFFTTLALQIFINNWAEGM
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RYSIETVGFSLLILANXILFKYGEARWYLPTISMYALALYRILPSVTGVISYYNEIA
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KIALIGHSGCCKSTLDDIIMGIPPLDSHKRITLINSNYALLXSKRRVLKNRNLTLQKGQ
KIALIGHSGCCKSTLDDIIMGIPPLDIIMGIPPLDNIYLLTSENRSWRKKIGYIPQNIYL
FDGTVGDNIAFGSAILDDIIMGIPPLDIIMCHTSCHEGGLKTQVGEGGGALLSGORQKI
GIRRALYDNPEILLVLDBATSALDNETESKIMDBIYQIAKNKTLIVIAHRLSTIERCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD06705.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / LEGICAL AND LEYSEVELIPETERNIHAVAGHDLSGAIFCDLFAGTGIVGET
FKKAVNKVISNDLEYYSFVLNGNYIGNIQEIPNKEELINKINSVALKKGFIYSHYSLG
GSSRQYFSETHAACLIDANRLKIEELKLSGNIDHHSYYFLLASLLESDKVANTASVYG
AFKRLKKAAQKELILKGAHFDVSLINANEVYQDSNDLIGKISGDILYLDPFYNARQY
GANYHLLKHTAAYILAYFPFFFFKKYDLPSVQKSFCSFFQILNAFENLIKKARFFYIFLSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to H. pylori 26695 gene HP1207"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to H. pylori 26695 gene HP1208"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'transī table=11
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(METHYLTRANSFERASE)"
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complement (6692. .7207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4110. .4778) /gene="jhp1130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4110. .4778)
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                      hp1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="jhp1130"
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                                                   365. .4101
gene="jhp1129"
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                                                                                                                       'codon start=1
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  gene
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HTG 24-MAR-2004

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CE 2 [bases 1 to 184688]

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Birren, B., Campoblano, A., Chang, J., Chazaro, B., Chocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Garadyna, S., Ginde, S., Gord, S., Goyette, M., Hollme, W., Illav, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landerst, L., Landerst, T., Lehocky, J., Levine, R., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McGund, C., McGonald, P., Major, J., Marquis, N., Maldrim, J., Norman, C.H., O'Connor, T., O'Donnell, P., Noylor, C., Norman, C.H., Co'Connor, T., O'Donnell, P., Pollara, V., Rawond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Reback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Travis, N., Triglilo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wilson, D., Ye, W.J., Young, G., Lander, M., Subramenian, R., and Zody, M., Vell, R., Woll, M., Subramer, A., and Zody, M., Direct Submission
                                                                         Helicobacter pylori
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 184688)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 14, clone RP24-14314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 184688)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC102439 194688 bp DNA linear Mus musculus chromosome 14 clone RP24-14314 map 14, IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                         Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Procein-protein interactions in Helicobacter pylori Patent: WO 02066501. A 5598 29-AUG-2002; Hybrigenics (FR) INSTITUT PASTEUR (FR) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC102439.3 GI:45680590
HTG; HTGS PHASB1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house moüse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25.4; DB 6;
Pred. No. 2.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                     /organism="Helicobacter pylori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTAATATTATTCAATAATATTGCTCAC 28
                                                                                                                     Helicobacteraceae; Helicobacter.
  GI:32958581
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.3%;
                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Conservative
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    AX793134.1
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Chow,T.P., Fry,K.B., Lim,M.Y. and Mcatee,C.P.
Antigenic composition and method of detection for Helicobacter
patent: JP 2001517091-A 332 02-0CT-2001;
Patent: JP 2001517091-A 332 02-0CT-2001;
PP 25-APR-1999 US 60/045107,14-0CT-1997 US 60/061958 PI
THERESA P CHOW,KIRK E FRY,MOON Y LIM,C P MCATEE PC
C12N15/31,C07K14/205,C07K16/12,A61K39/106
CC Strandedness: Single;
CC Topology: Linear;
FH Key
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PP 25-APR-1998 JP 1998547263
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THEREA P CHOW, KIRK E FRY, MOON Y LIM, C P MCATEE PC C12N15/31, C07K14/205, C07K16/12, A61K39/106
CC Strandedness: Single;
CC Topology: Linear;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 5598 from Patent WO02066501.
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BD061998.1 GI:22607603
JP 2001517091-A/332.
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Sirren, B., Lintcon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastlen, V., Boguslawkiy, L., Bouthgalter, B., Anderson, S., Cangalolano, A., Chang, J., Chazaro, B., Choese, Y., Camarata, J., Cangalolano, A., Chang, J., Chararo, B., Choese, P., Colangelo, M., Colling, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Paro, S., Govette, M., Gage, D., Galegan, J., Gardyna, S., Gord, S., Govette, M., Minne, M., Lilev, I., Ohnson, R., Dodge, S., Paro, S., Goode, S., Govette, M., Graham, L., Grand-Pletre, N., Gord, S., Govette, M., Marquis, M., Mattus, M., Schaler, C., Mattus, M., Subramian, P., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Ryman, G., Teedey, P., Spencer, B., Stange-Thoman, W., Trevers, M., Travers, M., Tradis, M., Mattus, M., Subramian, M., Travers, M., Traver
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Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Dases 1 to 21295)

5 Shiren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Cornis, B., DeArellano, K., Dodge, S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Plerre, M., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Maccarthy, M., Maldrim, J., Mencus, L., Mihova, T., Malenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Oconnor, P., O'Donnell, P., Nguyen, C., Nicol, R., Phunkhang, P., Pierre, N.,
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                              Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 3, clone RP23-335P23
       Mus musculus (house mouse)
Mus musculus
                                                                                                                                                  (bases 1 to 212995)
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2 (bases 1 to 212995)
          SOURCE
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Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamar, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Menneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connerl, P., Pierre, N.,
Nguyen, C., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seamen, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanović, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zalmon, J., Zammer, A. and Zody, M.
Direct Subfussion,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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------ Project Information
Center project name: 118796
Center clone name: 143_1_4
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/clone_lib="RPCI-24 Male Mouse BAC"
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Web Bite: http://www-seg.wi.mit.edu
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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Best Local Similarity 89.3
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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubba, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L. Submitted (28-0AN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 28, 2004 this sequence version replaced gi:38524693.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftb.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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1. . 2010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement [930. .1069)
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complement (4796. .4886)
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omplement (4912. .4981)
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6108. .6230
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rpt_family="MIR3"
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilidae; Lo 120194)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.8%; Score 23.2; DB 10; Best Local Similarity 89.3%; Pred. No. 1.5e+02; Matches 25; Conservative 0; Mismatches 3;
                                                                                                                                                                                /note="aingle clone coverage"
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/rpt_family="ORRID"
13853, .14253
/rpt_family="MTA"
14554, .14329
/rpt_family="MTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22532 TAATATTATTCAATAATATTGTTTAAAA 22505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt family="ID_B1"
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8955 .8992

/YPC family="(TTA)n"

/YPC family="ID_B1"

12006 .12006 .12006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7402. .17453
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7760. .17950
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                                                                                                                                                                                                                                                                                                                                                                                        16132. 16240
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RESULT 14
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E (Dases 1 to 16686)

E (Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H., Gelniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H., Baldwin,D., Banzon,J., Davenork,Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenort,L.B., Dietz,S.M., Carlson,J.W., Center,A., Champe,M., Davenort,L.B., Dietz,S.M., Ferifer,E., Galle,R.F., Gargy,N.S., George,K.A., Gonzalez,M., Houck,J., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIncosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,R.A., Nunco,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Saveri,J.S., Saith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 3R, region 87B-87B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC009741 166863 bp DNA linear INV 22-FEB-2001
Drosophila melanogaster, chromosome 3R, region 87B-87B, BAC clone
BACK4K17, complete sequence.
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Lawrence Berkeley, National Laboratory, MS 64-121
Berkeley, CA 94120
This sequence was assembled using end sequences from a whole genome
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Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD USA
This sequence was identified as CDM:10209984 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.5%; Score 22.8; DB 2; 92.3%; Pred. No. 2.4e+02;
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AC009741.5 GI:13096041
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Best Local Similarity 92.3
Matches 24; Conservative
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Drosophila melanogaster (Kruit Liy)

Drosophila melanogaster (Kruit Liy)

Brachycera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Ephydroidea; Drosophilade; Drosophila

Sphydroidea; Drosophila (Grambar, C.A., Gocayne, J.D., Andamel, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Andamel, M.D., Celniker, S.E., Richards, S., Ashburner, M., Henderson, S.N., Burton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Hell, G., Nelson, C.R., Gabor, G.L., Abril, J.F., Agbayani, A. M.H. J., Andrews-Pfannkoch, C., Baddwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Ballew, R.M., Bavendale, J., Bayraktaroglu, L., Beasley, E.M., Bandari, J., Border, P.D., Dew, I., Davis, P., Carbard, M., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Burtis, R.C., Busam, D.A., Butler, H., Cadleu, E., Center, A., Cherris, J., Gebblakov, S., Delcher, A., Deng, Z., Mays, A.D., Dew, I. Davises, P. W., Bebblos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I. Davises, P., Harris, M., Maller, S., Gorrell, J. H., Gu, Z., Gelbart, W.M., Glasser, K., Glong, F., Gorrell, J. H., Gu, Z., Gelbart, W.M., Glasser, K., Glong, F., Gorrell, J. H., Gu, Z., Gelbart, W.M., Glasser, K., Glong, F., Gorrell, J. H., Gu, Z., Mays, M.H., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hostnon, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liagy, Y., Lih, K., Kimmel, B.E., K., Karpen, G., Morne, M., Muzny, D.M., Nelson, D.L., Nelson, D.K., Nelson, R., Pittman, G.S., Pan, S., Pollard, J., Work, M., Pittman, G.S., Pan, S., Pollard, J., Work, M., Pittman, S., Saunders, R., Saunders, R., Tector, C., Turner, R., Stapleton, M., Skupsker, M., Skupsker, Saun, E., Starder, E., Starder, E., Starder, E., Starder, E., Starder, C., Terer, C., Terer, C., Terer,
shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Location/Qualifiers
1. .166863
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Drosophila melanogaster chromosome 3R, section 33 of 118 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 22.8; DB 3; Length 16
92.3%; Pred. No. 2.2e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                          organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="BACR44K17 (D976)"
                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="3R"
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AE003695 AE002708 AE014297
AE003695.2 GI:23171087
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Best Local Similarity 92.3%,
Local 24; Conservative
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/product="Cost as as a transparent products to a cost as a cost a cost as a cost as a cost 
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/locum taga:"GG4860"
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complement(join(16037. .17145,17276. .17515,17577. .17623))
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complement(join(11815, .12113,13041, .13706,13766, .14823,
4892. .15574,15631. .15850))
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Adams, M.D., Celliker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Ralpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Fise, E.,
Hodgson, A., George, K.A., Hoskins, R.A., Laverty, T., Muzny, D.M.,
Nelson, C.R., Pacleb, J.M., Park, S., Pfeiffer, B.D., Richards, S.,
Sodergern, E.J., Svirskas, R., Tabor, P.E., Wan, K., Stapleton, M.,
Sutton, G.G., Venter, C., Weinstock, G., Scherer, S.E., Myers, E.W.,
Gibbs, R.A. and Rubin, G.M.
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Submitted (10-MAR-2004) FlyBase, Harvard University, Biological
Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA
On Sep 18, 2002 this sequence version replaced gi:7299572.
Location/Qualifiers
Venter, E., Wang, A. H., Wang, X., Wang, Z. Y., Wassarman, D. A., Weinstock, G.M., Weissenbach, J., Williams, S.M., WoodageT, Worley, K.C., Wu, D., Yang, S., Yao, Q. A., Ye, J., Yeh, R.F., Zaveri, J. S., Zhan, M., Zhang, G., Zhoo, Q., Zheng, L., Zheng, X., Zhong, F.N., Zhong, W., Zhou, X., Zhu, X., Shith, H.O., Gibbs, R. A., Myers, E. W., Rubin, G. M. and Venter, J. C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finishing a whole-genome shotgun: release 3 of the Drosophila melanogater euchtromatic genome sequence Genome Biol. 3 (12), RESEARCH0079 (2002)
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Marninker, J.S., Bergman, C.M., Kronmiller, B., Carlson, J.,
Svirskas, R., Patel, S., Frise, E., Wheeler, D.A., Lewis, S.E.,
Rubin, G.M., Ashburner, M. and Celniker, S.E.
The transposable elements of the Drosophila melanogaster
euchromatin: a genomics perspective
Genome Biol. 3 (12), RESEARCH0084 (2002)
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/note="CR31356-RA"
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of BX571856 from base 600001 (BX571856 Staphylococcus aureus subs
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Continuation (7 of 29)
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Search completed: April 24, 2005, 03:21:56 Job time: 806.69 secs

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This 3' primer is used with a 5' primer (see AAV07971) in the PCR amplification of Helicobacter, e.g. Helicobacter, genomic DNA in order to obtain DNA (see AAV07964) encoding the a 50 kDa polypeptide (see AAW73055) designated GHPO 750. The isolated polynucleotide, and encoded
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Adg08665 Ciona int
Aaa79704 Eucalyptu
Aah76178 A. thalia
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Aav07970 Helicobac
Aav0796 Helicobac
Aav90742 Nucleotid
Aav90873 Nucleotid
Abx65371 Novel Hel
Abx65371 Novel Hel
Abx653781 Helicobac
Aav7968 Helicobac
Abr79830 Fungal ZB
Abr79830 Fungal ZB
Abz10049 Haematopo
Abz10195 Haematopo
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Aah76176 A. thalia
Adr08103 Full leng
Abl12454 Drosophil
Abl33002 Human imm
Aah20175 Mouse spa
Acnf5118 Human gen
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Abn7026 Streptoco
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ALIGNMENTS

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases. GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR; Ä Algarawi Helicobacter pylori polypeptide GHPO 750 3' DNA primer. ပဲ (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC. Miller Tomb J, Claim 5, Page 156; 184pp; English. B 98WO-US006421 97US-00831310. 97US-00834666. AAV07972 Btandard; DNA; 31 (revised)
(first entry) Lissolo L, WPI; 1998-568251/48. Synthetic. Helicobacter pylori

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AAV07964/c
ID AAV07964 standard; DNA; 1448 BP.
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01-APR-1997;
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02-FEB-1999
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                                       AAV07964;
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 and
to correct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
                                                                                  Gaps
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polypeptide, can be used to develop vaccines for the treatment prevention of Helicobacter infections. (Updated on 25-MAR-2003
                                                           Query Match 100.0%; Score 31; DB 2; Length 31; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 31; 0.12;
                                                                                                                                                                                                                                                  Helicobacter pylori polypeptide GHPO 1360 5' DNA primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller C, Algarawi
                                         Sequence 31 BP; 12 A; 6 C; 2 G; 11 T; 0 U; 0 Other;
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                                                                                                     1 GCTAATATTATTCAATAATATTGCTCACAAC 31
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:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 156; 184pp; English.
                                                                                                                                                                            AAV07970 standard; DNA; 31 BP
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                                                                                                                                                                                                                                                                                                     Synthetic.
Helicobacter pylori
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Matches
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This DNA sequence codes for a 50 kDa Helicobacter pylori polypeptide (see AAW73035) designated GHPO 750. A polynucleotide encoding GHPO 750 can be obtained from genomic DNA by PCR amplification (see AAW0791-72. The invention provides polynucleotides (see AAW072001, AAW07912-21 and AAW07963-64) encoding a family 76 kDa Helicobacter polypeptides (see AAW33022-32), GHPO 750 and a 32 kDa polypeptide (see AAW3303). These CC AAW73022-32), GHPO 750 and a 32 kDa polypeptide (see AAW3303). These CC polynucleotides were initially identified in a search of H. pylori C genomic databases. DNA cassettes for expression of the Helicobacter proteins (unprocessed or mature forms) in prokaryotic or eukaryotic cells are provided. The polynucleotides can be used in vacciness to prevent or treat Hb infection in a mammal. Viral (especially poxvirus) or bacterial vectors are used. Products and methods of the invention allow treatment and prevention of gastroducdenal diseases associated with Hb infections, concluding acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and dudenal ulcers. Diagnostic and detection methods are also provided. GHPO 750 was demonstrated to be a protective contien. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                        GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; ss.
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                                                                          Helicobacter pylori 50 kDa polypeptide GHPO 750 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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97US-00834666.
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                                                                                                                                                                                                                                      Helicobacter pylori.
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20-MAR-2003 18-FEB-1999

AAV90742;

05-NOV-1998,

Chow TP,

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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody detection assays, on sera, plasma, urine, saliva etc., they are highly ensetitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                     New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response.
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PCR; primer; 88.
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                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Legrain P, Rain J, Colland F,
                                                                                                     98WO-US008487.
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                                                                                                                                               97US-0045107P
                                                                                                                                                                     97US-0061958P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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es 30, Conservative
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(INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                               WPI; 1999-009433/01.
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                                                                                                                                                                                                                                                     Chow TP, Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200266501-A2.
                      WO9849314-A2
                                                                                                       25-APR-1998;
                                                                                                                                                 25-APR-1997;
                                                                                                                                                                   14-OCT-1997;
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                                                             05-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoceactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly ensisted and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gantric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Helicobacter pylori antigens and related nucleic acid sequences -
useful in serological diagnosis and protective vaccines, providing long-
lasting immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                       Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 94.8%; Score 29.4; DB 2; Length 968; 1. Similarity 96.8%; Pred. No. 0.42; 30; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 968 BP; 306 A; 154 C; 260 G; 248 T; 0 U; 0 Other;
                                                                                                                                                 Nucleotide sequence of clone Z14.ASM from cluster 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTAATATTTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Page 170; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENELABS TECHNOLOGIES INC.
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AAV90742 standard; DNA; 968 BP.
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                                                                                      (revised)
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                                                                                                                                                                                                                                                       Helicobacter pylori
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18-FEB-1999
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AAV90873;

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Query Match

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Length 970;

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us-10-039-183a-17.rng

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themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic proteins used in proliferation, or express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic callular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or e
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                          Sequence 1200 BP; 365 A; 207 C; 319 G; 309 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           77.4%; Score 24; DB 4;
100.0%; Pred. No. 34;
iive 0; Mismatches 0
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; SEQ ID NO 22730; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       860/c
ACA34860 standard; DNA; 1200
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                24; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                               Local Similarity
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Wall D,
                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                       The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence represents a primer used to isolate polymucleotides encoding Helicobacter pylori proteins for studies on protein-protein interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes
                                        New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori DNA for cellular proliferation protein #135.
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                                                                                                                                                                                                                                                                                                                           Score 25.4; DB 6; Length 30;
Pred. No. 11;
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                                                                                                                                                                                                                                                                                               Sequence 30 BP; 10 A; 7 C; 1 G; 9 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                          Example 9; Page 561; 642pp; English.
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AAS53681/c
ID AAS53681 standard; DNA; 1200 BP.
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23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0255625P.
22-DEC-2000; 2000US-0255931P.
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2000US-0206848P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu HH;
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     WPI; 2002-674910/72.
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 24; Conserv
                                                                         ulcers in mammals.
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23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002
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screening

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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compounds acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the artisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the confict of identifying proteins or screening for homologous nucleic acids required for proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, confirm discovery programs, or for screening homologous nucleic acids acids required for proliferation in cells other than S. aureus, S. typhimurium, and the strain of the printed specification, but was obtained in cells of the confirm part of the printed specification, but was obtained in the confirm that the confirm the confirmition of the printed specification, but was obtained in the confirmition of the printed specification, but was obtained in the confirmition of the confirmition of the printed specification, but we confirm the confirmition of the printed specification and the confirmition of the printed specification of the printed specification and the confirmition of the conf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.4%; Score 24; DB 100.0%; Pred. No. 34; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US006421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kleanthous H,
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                                                           This 3' primer was used with a 5' primer (see AAV07967) in the PCR amplification of Helicobacter pylori strain ORV2001 genomic DNA in order to obtain DNA (see AAV07964) encoding a 50 kDa polypeptide (see AAW73035) designated GHPO 750. The primer pair includes a 5' clamp and Bamil and XhoI restriction enzyme reocquition equences for cloning purposes. The PCR product was ligated into vector pET28a, and recombinant polypeptide was expressed as a histidine-tagged fusion protein in B. coli host cells. The polypeptide can be used to develop vaccines for the treatment and prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein, antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliocan synthase inhibitor; gliocan synthase inhibitor; gliocan; fungal toxin; cell surface receptor; plant growth regulator; plantorin; insecticide; antineoplastic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation the expression of at least one zinc binuclear cluster protein gene.
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                                                                                                                                                                                                                                                                                                                                  Score 21.6; DB 2; Length 30;
Pred. No. 2.4e+02;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                             Sequence 30 BP; 8 A; 8 C; 4 G; 10 T; 0 U; 0 Other;
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                                       Example 3.B; Page 64; 184pp; English.
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gastroduodenal diseases.
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P-PSDB; ABP35641.
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Best Local Si
Matches 24;
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Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; amevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; anglogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; call surface receptor; plant growth regulator; pigment; insecticide; antineoplastic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene.
an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a medulator of cell surface receptor signalling, a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a equivalent amounts of the fermentor required for the production of biomass required for the production of biomass required for the production, which translates into decreased waste that must be handled in downstream processing. The sequences given in records ABN7974-ABN79911 represent ZBC genes of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                         67.7%; Score 21; DB 6; Length 2595; 82.8%; Pred. No. 3.8e+02; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                        Sequence 2595 BP; 829 A; 588 C; 491 G; 687 T; 0 U; 0 Other;
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Matches 24; Conservative
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P-PSDB; ABP35642.
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metabolite by a fungus. This involves modulating the expression of at least one 2EC (Sinc binuclear clueter protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such

The invention relates to improving the production of a secondary

Claim 2; SEQ ID NO 147; 49pp + Sequence Listing; English.

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as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling, a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decreased in records ABN/9764-ABN/9911 represent ZBC genes of the invention. Note: The sequence data for this patent did not form part of the printed for this patent did not form part of the printed for the control of the printed directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09661 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: differentiating between healthy haematopoietic cells and proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, comprises contacting a target nucleic acid with a reagent tl
distinguishes between methylated and non-methylated CpG dinucleotides.
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G, Lesche R, Leu E;
Mueller V, Otto T, I
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Pred. No. 3.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                    1027 CTAATACTAAACAATAATATTACTCATAA 1055
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Olek A, Piepenbrock C, Adorjan P, Grabs
Lewin A, Lipscher E, Maier S, Model F,
Schwope I, Ziebarth H,
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                               67.78;
                                                                                                                                                                                                                                                                                                                                  82.8%;
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                                                                                                                                                                                                                                                                                                                                                       24; Conservative
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Schwope I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ10049;
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                         lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single mucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements, and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a prediaposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables thighly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haematopoietic cell proliferation disorder related DNA sequence #335.
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G, Leache R, Leu E;
Mueller V, Otto T, I
haematopoietic cells, for differentiating between acute
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Olek A, Piepenbrock C, Adorjan P, Grabs G,
Lewin A, Lippscher E, Maier S, Model F, Mue
Schwope I, Ziebarth H;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; archritis; arteriosclerosis; anti-HIV; neuroprotective; antiarchritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
           lymphocytic leukaemia and acut, myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nuclectide polymorphisms (SNPs) of haematopoletic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoletic cell proliferation disorder related by sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoletic cell proliferative disorders. The present method enables highly specific classification of haematopoletic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                  Gapa
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haematopoietic cells; for differentiating between acute
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                                                                                                                                                                                                                                       Sequence 5333 BP; 1248 A; 0 C; 1254 G; 2831 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             Length 5333;
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Pred. No. 3.8e+02;
0; Mismatches 5;
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2000DE-01032529.
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                                                                                                                                                                                                                                                                                               Local Similarity
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DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, asing, glomeraliar disease, Lewy body disease, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV; anticonvulsant, ophthalmological, antiarthritic; antidabetic, antipsoriatic, antiantilametory, cancer; eye disease; arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease; AIDS; epilepsy, neurofibromatosis, rheumatoid arthritis; psoriasis; bowel disease; gene,
                                                                                                                                                                                                             Gaps
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                                                                                                                                                   Sequence 8333 BP; 1968 A; 183 C; 2037 G; 4145 T; 0 U; 0 Other;
                                                                                                                                                                             Query Match 67.7%; Score 21; DB 4; Length 8333; Best Local Similarity 82.8%; Pred. No. 3.8e+02; Matches 24; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 1475.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid thetkaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention

Seguence 8333 BP, 1968 A; 183 C; 2037 G; 4145 T; 0 U; 0 Other;

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

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Berlin

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2002-130909/17

Claim 1; SEQ ID NO 1475; 32pp + Sequence Listing; German.

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            Length 8333;
                      3.8e+02;
         Score 21; DB 6;
Pred. No. 3.8e+02
67.7%; Scor.
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0; Mismatches
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Matches 24; Conserv
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NAME/KEY: misc_feature
US-09-949-016-13922/c
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ORGANISM: Human
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Sequence 14700, A
Sequence 14701, A
Sequence 14702, A
Sequence 14703, A
Sequence 13635, A
Sequence 13635, A
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856, App
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15466, A
15922, A
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                                                                                                       April 24, 2005, 00:51:24; Search time 60.2535 Seconds (without alignments) 841.853 Million cell updates/sec
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Sequence 13924,
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Sequence 13926,
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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5-09-949-016-15466
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               GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
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Sequence 13922, Application US/09949016

Sequence 13922, Application US/09949016

Sequence 13922, Application US/09949016

Sequence 13922, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECSED OF Windows Version 4.0

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LENGTH: 278866
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is Sequence 13923, Application US/09949016
is Sequence 13923, Application US/09949016
is Patent No. 6812339
is GENERAL INFORMATION:
is APPLICANTY UNIVERSE, J. Craig et al.
itTILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
is TILE REPERENCE: CL001307
is CURRENT APPLICATION NUMBER: US/09/949,016
is CURRENT PILING DATE: 2000-04-14
is PRIOR APPLICATION NUMBER: 60/241,755
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US-09-949-016-13504

US-09-949-016-131358

US-09-949-016-16138

US-09-949-016-16138

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; OTHER INFORMATION: n = A,T,C or US-09-949-016-13922
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Best Local Similarity 85.7%
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DB 4;
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69.7%; Score 21.6; I
Best Local Similarity 85.7%; Pred. No. 40;
Matches 24; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
STORMARE: PRESIZE FILING DATE: 2000-10-03
COUNTRY FILING DA
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; Sequence 14699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION;
; APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Sequence 13926, Application US/09949016
; Patent No. 6812339
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13926
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| LOCATION: (1)...(278866)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13925
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Best Local Similarity 85.73
Matches 24; Conservative
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LENGTH: 278866
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Sequence 13924, Application US/09949016

Sequence 13924, Application US/09949016

Sequence 13924, Application US/09949016

Sequence 13924, Application US/0949016

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOFTWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 13924

LENGTH: 278866
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Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, D. Craig et al.
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PLILATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SQCTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 13923
LENGTH: 278866
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) LOCATION: (1)...(27866)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13923
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Best Local Similarity 85.7%; Pred. No. 40;
Matches. 24; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14702
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Patent No. 6812339
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14701
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702
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LENGTH: 278866
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-14-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 40;
0; Mismatches
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                                         TILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PEDICATION NUMBER: 60/241,755
PRIOR PEDICATION NUMBER: 60/237,768
PRIOR PELING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PREESEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14700
LENGTH: 278866
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Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14700
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14699
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Best Local Similarity 85.7%;
Matches 24; Conservative
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Best Local Similarity 85.7°
Matches 24, Conservative
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ORGANISM: Human
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LENGTH: 278866
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; Sequence 14701, Application US/09949016

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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-00-03

PRIOR PLING DATE: 2000-09

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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US-10-101-464A-856
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                                                                   SERVERAL INFORMATION:

APPLICANT: URITER, J. Craig et al.

APPLICANT: URITER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PESESEQ for Windows Version 4.0

SEQ ID NO 14703

LENGTH: 278866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOFTWARE: RESEREQ FOR WINDOWS VERSION 4.0
SSO ID NO 13635
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Pred. No. 40;
0; Mismatches 4; Indels 0;
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US-09-949-016-14703/c
; Sequence 14703, Application US/09949016
; Patent No. 6812339
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

| LOCATION: (1)...(278866)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14703
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Best Local Similarity 85.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 80.0
hes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
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Matches
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RESULT 12

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Sequence 317, Application US/09422978

Sequence 317, Application US/09422978

Sequence No. 6537751

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, IJya

APPLICANT: Chumakov, IJya

CURRENT Blumenfeld, Marta

APLICANT: Chumakov, IJya

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US/09/22,978

EARLIER PELICATION NUMBER: US/09/21

EARLIER PELICATION NUMBER: US/0/109,732

EARLIER APPLICATION NUMBER: US/0/109,732

EARLIER APPLICATION NUMBER: US/0/109,732

EARLIER APPLICATION NUMBER: US/0/109,732

SEALIER PILING DATE: 1999-104-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 317

TENGTH. 47
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GENERAL INPORTION:
GENERAL INPORTION:
GENERAL INPORTION:
GENERAL GENERAL INPORTION:
GENERAL APPLICATION NUMBER:
GENERAL FILING DATE:
GOOG-03-18
FRIOR FILING DATE:
1999-01-12
FRIOR FILING DATE:
1999-01-12
FRIOR FILING DATE:
1999-01-01
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
COATION: 24
COTHER INFORMATION: 99-14186-424 : polymorphic base A or US-09-422-978-31
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88.0%;
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Best Local Similarity 81.5%;
Matches 22; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 22; Conserv
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15466
SEQ ID NO 15466
SEQ ID NO 15466
SEQ ID NO 15466
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       Sequence 3, Application US/09693205A

Fatent No. 681233

GENERAL INFORMATION:

APPLICANT: Hudson, Thomas J.

APPLICANT: Richter, James C.

APPLICANT: Richter, Andrea

TITLE OF INVENTION: INENTIFICATION OF ARSACS MUTATIONS AND TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 2825.1021-003

CURRENT APPLICATION NUMBER: US/09/693,205A

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 60/160,588

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 3

SEC ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

64.5%; Score 20; DB 4; Length 11492;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels
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Best Local Similarity 82.19
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-949-016-15466/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15466
US-09-693-205A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 11492
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Search completed: April 24, 2005, 05:33:14 Job time : 64.4535 secs

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Sequence 71415. A Sequence 856, App Sequence 856, App Sequence 31, Appli

Sequence 975, App Sequence 1906, Ap Sequence 6, Appli

Sequence 166131, Sequence 22, Appl Sequence 57, Appl Sequence 317, App

Scoring table:

Searched:

Database

Perfect score:

Sequence:

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Run on:

113, App 1475, Ap

Sequence 1 Sequence 1 Sequence 2

Sequence Sequence Sequence Sequence

Sequence 1 Sequence 3 Sequence 1

Sequence

Sequence 1, Appli Sequence 15, Appli Sequence 15, App Sequence 692, App Sequence 435, Appli Sequence 5, Appli Sequence 13, Appli

5, Appli 13, Appl 9, Appli

Sequence 1

Sequence

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US-08-831-310-15

Sequence 15, Application US/08831310

PUDLication No. US/020020035A1

PUDLication No. US/020020035A1

GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold et al.

TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP
              US-10-149-310-145

US-10-149-310-147

US-10-473-126-335

US-10-473-126-335

US-10-473-126-335

US-10-239-676-113

US-10-240-453-129

US-10-425-114-24648

US-10-425-114-25834

US-10-425-114-27834

US-10-425-114-27834

US-10-425-115-166131

US-10-425-115-166131

US-10-175-52-57

US-10-175-52-57

US-10-175-52-856

US-10-101-464A-856

US-10-203-351-3

US-10-203-351-3

US-10-203-351-3

US-10-101-464A-856

US-10-101-464A-856

US-10-203-351-3

US-10-203-351-3

US-10-101-464A-856

US-10-203-351-3
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15 US-10-084-817-315

10 US-09-966-706-692

10 US-09-813-319-435

15 US-10-286-152A-5

17 US-10-36-345-13

17 US-10-36-345-13

17 US-10-36-26-1327

17 US-10-062-674-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-790-988-1
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STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 0613;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
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87394
640681
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Sequence 17, Appl
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Sequence 17, Appl
Sequence 3, Appli
Sequence 32, Appli
Sequence 32, Appl
Sequence 7318, Ap
Sequence 2730, Ap
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                                                                                                                                April 24, 2005, 02:04:39 ; Search time 250.62 Seconds (without alignments) 750.949 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-811-310-3

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9 US-10-622-126-32

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US-10-282-122A-22730
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US-10-039-183A-8
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US-08-831-310-17
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Maximum Match 100%
Listing first 45 summaries
                                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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US-10-039-183A-15
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Sequence 17, Application US/08831310
Sequence 17, Application US/08831310
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KLeanthous, Harlochacter GHPO 1360 and
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES:
ADDRESSEE: Clark & Elbing LLP
STRET: 176 Federal Street
CITT: Boston
STATE: MA
CONNTRY: USA
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                                                                                                                                                   Query Match 100.0%; Score 31; DB 8; Length 31; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 31; Conservative 0; Mismatches 0; Indels
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ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REGISTRATION NUMBER: 30,175
REGISTRATION NUMBER: 06132/037001
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 31; DB 8; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 31; Conservative 0; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 bases pairs
LYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                    ; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGGY: linear
US-08-831-310-15
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TOPOLOGY: linear

US-08-831-310-17
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US-10-039-183A-15
; Sequence 15, Application US/10039183A
; Publication No. US20030143242A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Lissolo, Ling

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US-10-39-183A-17

US-10-039-183A-17

Sequence 17, Application US/10039183A

Publication No. US20030143242A1

GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold

APPLICANT: Inseed, Ling

APPLICANT: Milest. Charles

TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750

TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750

TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules

TILE REPRENCE: 06132/037002

CURRENT APPLICATION NUMBER: US/10/039,183A

CURRENT APPLICATION NUMBER: US 08/831,310

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 31

LENGTH: 31
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US-08-831-310-3/c
is Sequence 3, Application US/08831310
j Sequence 3, Application US/08831310
j Publication No. US2020026035A1
j Publication No. US20020026035A1
j Publication No. US20020026035A1
j TILE OF INVENTION: Helicobacter GHPO 1360 and
j TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
j NUMBER OF SEQUENCES: 18
j CORRESPONDENCE ADDRESS:
j STREET: 176 Federal Street
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: POLYPEPTIGES and Corresponding Polymucleotide Molecules
FILE REFERENCE: 06132/037002
CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT APPLICATION NUMBER: US 08/831,310
PRIOR APPLICATION NUMBER: US 08/831,310
PRIOR APPLICATION NUMBER: US 08/831,310
PRIOR PILING DATE: 1997-04-01
SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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100.0%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 31; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.19;
trive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Helicobacter pylori
US-10-039-183A-17
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Best Local Similarity 100.
Matches 31; Conservative
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31; Conservative
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Matches 31; Conservative
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APPLICANT: Tomb. Jean-Francois
APPLICANT: Tomb. Jean-Francois
APPLICANT: Tomb. Jean-Francois
APPLICANT: Millar, Charles
APPLICANT: Millar, Charles
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: POlypeptides and Corresponding Polymucleotide Molecules
FILE REFERENCE: 06132/037002
CURRENT FILING DATE: 2002-12-13
FRICK PILING DATE: 1002-12-13
PRIOR PILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1448
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                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATURG SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: US-08/831,310
FILING DA
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100.0%; Pred. No. 0.33;
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                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence (CCATION: 118...1314 CTHER INFORMATION: US-08-831-310-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (118)...(1314)
US-10-039-183A-3
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Best Local Similarity
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| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Knapp, Bernhard |
| APPLICANT: Knapp, Bernhard |
| APPLICANT: Hundt, Erika |
| APPLICANT: Schmidt, Karl-Heinz |
| TITLE OF INVENTION: Proteins, In Particular Membrane Proteins, of |
| TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use |
| TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use |
| TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use |
| TITLE OF INVENTION WUMBER: US/10/662,126 |
| CURRENT FILING DATE: 2003-09-12 |
| PRIOR PLICATION NUMBER: PCT/IB97/00981 |
| PRIOR PLICATION NUMBER: PCT/IB97/00981 |
| PRIOR FILING DATE: 1999-01-19 |
| PRIOR FILING DATE: 1999-01-19 |
| SOFTWARE: Patentin Ver: 2.1 |
| SEQ. ID NO 32
Gaps
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LOCATION: (891)..(2090)
OTHER INFORMATION: bp protein; 42 kD protein from Helicobacter pylori
US-10-662-126-32
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APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Will Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
Indela
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                                                                                                                   1324 GCTAATATTATTCAATAATATTGCTCACAAC 1294
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                                                         1 GCTAATATTATTCAATAATATTGCTCACAAC 31
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0; Mismatches
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PRING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
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                                                                                                                                                                                                                                      US-10-662-126-32/c
; Sequence 32, Application US/10662126
; Publication No. US20050063987A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Helicobacter pylori
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Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
Matches 24; Conserv
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STATE: MA
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STRANDEDNESS:
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US-08-831-310-8
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## TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
## CURRENT APPLICATION NUMBER: US/10/282,122A

## CURRENT PILING DATE: 2003-02-20

## READR APPLICATION NUMBER: 60/204,948

## REIOR FILING DATE: 2000-05-23

## RIOR PELICATION NUMBER: 60/206,848

## REIOR FILING DATE: 2000-05-23

## RIOR PELICATION NUMBER: 60/207,727

## RIOR PELICATION NUMBER: 60/207,727

## RIOR PELICATION NUMBER: 60/203,335

## RIOR PELICATION NUMBER: 60/230,335

## RIOR PELICATION NUMBER: 60/230,335

## RIOR PELICATION NUMBER: 60/230,335

## RIOR PELICATION NUMBER: 60/230,336

## RIOR PELICATION NUMBER: 60/230,625

## RIOR PELICATION NUMBER: 60/253,625

## RIOR PELICATION NUMBER: 60/253,636

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87;
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 718
TENGTH: 1200
TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22730, Application US/10282122A
Sequence 22730, Application US/10282122A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Applicant: Chleen, Kari
APPLICANT: Ohleen, Kari
APPLICANT: Ohleen, Kari
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grant
APPLICANT: Yamamoco, Robert
APPLICANT: Yamamoco, Robert
APPLICANT: Yerryth, R.
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SEQ ID NO 22730
LENGTH: 1200
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; ORGANISM: Helicobacter pylori
US-10-282-122A-22730
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; NAME/KEY: CDS
; LOCATION: (1)...(1200)
US-09-815-242-7318
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APPLICANT:
APPLICANT:
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Sequence 8, Application US/08831310
Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
CORRESPONDENCE Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10039183A
Publication No. US20030143242A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REFERENCE: 06132/037002
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  DB 17; Length 1200;
87;
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                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 77.4%; Score 24; DB 1 Similarity 100.0%; Pred. No. 87; 24; Conservative 0; Mismatches
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                                                                                                          1200 TTATTCAATAATATTGCTCACAAC 1177
                                                                                 TTATTCAATAATATTGCTCACAAC 31
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STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110
COMPUTER READABLE FORM:
MEDUIN TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
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Best Local Similarity
Matches 24; Conserva
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US-10-473-126-189/c
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US-10-149-310-147
                           2595
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  SEQ ID NO 145
LENGTH: 259
                                                                                                                                     Query Match
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; Sequence 28120. Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Planta
; TITLE OF INVENTION: Planta
; TITLE OF INVENTION: Planta
; TITLE OF INVENTION: NUMBER: US/10/425,115
; CURRENT RILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO S 28120
; LENGTH: 1290
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APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Macon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Anir
TITLE OF INVENTION: Anic Binuclear Cluster Proteins
FILE REFERENCE: 14184-019031
CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT APPLICATION NUMBER: US/10/149,310
PRIOR RILING DATE: 2003-02-19
PRIOR PILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
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82.8%; Pred. No. 9.7e+02;
tive 0; Mismatches 5;
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US-10-425-115-28120
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CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 08/831,310
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                  1 GCTAATATTTCAATAATATTGCTCAC 28
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; Sequence 145. Application US/10149310
; Publication No. US20040077039A1
; GENERAL INFORMATION:
                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Helicobacter pylori
US-10-039-183A-8
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Best Local Similarity 82.8
Matches 24; Conservative
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                                                                                                                                                       LENGTH: 30
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Sequence 189, Application US/10473126
Publication VS20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 189
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Macon, Mary
APPLICANT: Macon, Mary
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
FILE REFERENCE: 14184-019U31
CURRENT APPLICATION NUMBER: DC7/US01/29288
FRICA APPLICATION NUMBER: PC7/US01/29288
FRICA FILING DATE: 2001-09-19
FRIOR FILING DATE: 2000-09-19
FRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFFWARE: Patentin version 3.1
SEQ ID NO 147
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Pred. No. 1.2e+03;
0; Mismatches 5; Indels
                                                                                              Score 21; DB 17; Length 2595; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 17; Length 2595; Pred. No. 1.1e+03; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Kluyveromyces marxianus var. lactis
US-10-149-310-147
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                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               Sequence 147, Application US/10149310
Publication No. US20040077039A1
GENERAL INFORMATION:
TYPE: DNA

CRGANISM: Kluyveromyces lactis
US-10-149-310-145
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82.8%;
                                                                                              67.7%;
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1 Similarity 82.8%;
24; Conservative (
                                                                                                                   Best Local Similarity 82.8
Matches 24; Conservative
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Matches 24; Conserva
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Search completed: April 24, 2005, 05:52:22 Job time : 252.62 secs

C 25 17.2 71.7 302 C 26 17.2 71.7 303 C 27 17.2 71.7 404 28 17.2 71.7 464	17.2 71.7 17.2 71.7 17.2 71.7	32 17.2 71.7 33 17.2 71.7 34 17.2 71.7	17.2 71.7 17.2 71.7 17.2 71.7	17.2 71.7	17.2 71.7	45 17.2 71.7			DEFINITION SP 0106 B1 F05 T7.	ACCESSION AZ206030 VERSION AZ206030.1 GI:84. KEYWORDS GSS. SOURCE Strongylocentrotu ORGANISM Strongylocentrotu ERARAYOGIS, SHEAD	Strongylocentroti REFERENCE 1 (bases 1 to 66. AUTHORS Cameron, R.A., Mah	wray, G.A., Ectens and Hood, L. TITLE A see archin geno	JOURNAL Proc. Natl. Acad.		California Institi Pasadena Californ	Tel: (626) 395-84: Fax: (626) 793-30	Email: acameron@c. Plate: 106 row:	Seq primer: T7 Class: BAC ends	High quality seque FEATURES Location	source 1663 /organis	/mol_typ /db_xref	/clone="	urchin, /note="0	DH10B"	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	ic - nucleic search, using sw model	April 24, 2005, 00:31:54; Search time 1271.32 Seconds (without alignments) 718.576 Million cell updates/sec	US-10-039-183A-18 score: 24 : 1 cataacgcaaataacgctacgcat 24	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	: 34239544 Beqs, 19032134700 residues	mber of hits satisfying chosen parameters: 68479088	DB seq length: 0 DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	: ES	3: 9D merc:* 4: 9D est3:* 5: 9D est4:* 6: 9D est5:* 7: 9D est5:* 9: 9D gss1:*	. eee .	SUMMARIES	Score Match Length DB ID Description	19.4 80.8 663 8 AZ20630 18.8 78.3 486 2 BE011185 BE011185 PM3-BN021 18.4 76.7 573 4 BI358245 BI358245 RE44953.5	76.7 614 4 B1577150 B1577150 76.7 621 4 B1363229 B1363229	76.7 641 4 BI172492 BI172492 76.7 674 4 BI231884 BI231884	76.7 1201 9 CNS0014B AL057687 75.8 488 2 BE225571 BE225571	75.8 731 8 CC111452 CC111452 74.2 617 9 DR6M14T AL737121	74.2 923 9 CNSO05B0 AL057860 73.3 533 1 AL915262 AL915262	73.3 646 7 CV105677 CV105677 73.3 671 9 CG796914 CG796914	.6 73.3 731 9 BX132281 BX132281 Danic .6 73.3 790 9 CC658434 CC658434 OGRB	.6 73.3 875 9 CL496111 CL496111	.4 72.5 945 9 CL985419 CL985419 .4 72.5 1080 9 CW000366 CW000366	17.4 72.5 1100 9 CL998017 CL998017 ZMMHFG01 17.2 71.7 182 2 BE707185 BE707185 MR2-HT044 17.2 71.7 276 2 B8402258 B8402258	
	OM nucleic	Run on:	Title: Perfect score Sequence:	Scoring	Searched	Total number	Minimum Maximum	Post-prc	Database		P1 8C		Result No.	- 12 E	4 N	9	ω σ υ υ	110		c 14		18 19	20	c 53 5	

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663 bp DNA linear GSS 31-AUG-2000 T7A Strongylocentrotus purpuratus, purple sea enomic BAC library Strongylocentrotus purpuratus late=106 Col=9 Row=L, genomic survey sequence.
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rpe="genomic DNA"

f="taxon:7668"
="Plate=106 Col=9 Row=L"
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, sperm genomic BAC library"
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BB070814 BB070814
CG842150 Ynhw2764
CN629723 taf59309.
BX609783 BX609783
CK498310 E8wbb0 00
BF208786 C187261
CN613483 C889E2701
CN629461 taf59409.
CN629967 AB L3 43A
AV400542 AV400542
BW189097042 BW99834
BW1897042 BW998934
BW183256 BW18326
AA543535 VK57C04.
EW134781 BW134781
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BW1860909 AZOZ.108A
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hairas,G., Rast,J.P., Martinez,P., Blondi,T.R.,
allace,J.C., Poustka,A.J., Livingston,B.T.,
nsohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
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roa, Echinodermata, Eleutherozoa; Echinozoa;
phinoidea; Echinoea; Echinoida;
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Ltute of Technology
rnia 91125, USA
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@caltech.edu
:: L column: 9
   BB070814
CC6842150
CC6842150
CC69723
BK609783
CCK498310
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EST 31-JUL-2001

ACCESSION VERSION KEYWORDS

DEFINITION

RESULT 2 BE011185 LOCUS

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SOURCE

REFERENCE AUTHORS

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Inote="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was Kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
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REA70793. Sprime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE70793 5 similar to BG:DSG1219.1: FBan0004482 GO:[] located on: 2L 35B9.
                           BI358245

BI44953. Sprime RE Drosophila melanogaster normalized Embryo pFlc-1
Drosophila melanogaster cDNA clane RE44953 5 similar to
BG:DS01219.1: FBBAN0004482 located on: 2L 35B9-35B9;: 05/13/2001,
                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Buoptera; Badopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 573)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Garlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Chavin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phounnenavong, S., Wan, K., Yu, C., Lewis, S.B., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab host="DHS-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized Embryo
PFIC-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 (49.98
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003645: arm:2L [14622887,14883853]
estimated-cyto:35B5-35B9: 05/13/2001
Plate: RE.449 row: E column: 5
High quality sequence stop: 495.
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Drosophila melanogaster
Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
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Pred. No. 1.5e+02;
0; Mismatches 1;
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BDGP/HHMI RE Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0218"
/clone_lib="BN0218"
/note="forgan: breast normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 486).

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=PM3-BN0218-100
500-003-e04&t3=2000-05-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 407.
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                                                                                                                                                                                                                                                                                              BE011185 486 bp mRNA linear EST 05-JUN-2000 PM3-BN0218-100500-003-e04 BN0218 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                           Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
        Length 663;
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        .,
     80.8%; Score 19.4; DB 95.2%; Pred. No. 47;
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Query Match 80.8:
Best Local Similarity 95.2
Matches 20; Conservative
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One Cyclotron Rd, Berkeley, CA 94720, USA
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821 bp mRNA linear EST 01-AUG-2003

8451990.5prime RE Drosophila melanogaster normalized Embryo pFlc-1

B10502phila melanogaster cDNA clone RE47990 5 similar to

B2105021219.1: FBan0004482 located on: 2L 3589-3589;: 05/13/2001,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Badopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilides; Drosophila.

1 (bases 1 to 621)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.B., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
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/clone="RE70793"
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/clone="Lib="RE Drosophila melanogaster normalized Embryo
Ephydroidea; Drosophilidae; Drosophila.

1 [bases 1 to 614)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Pholanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
htt genomic AE003645: arm:2L [14622887,14883853]
estimated-cyto:35B5-35B9: 05/17/2001
Plate: RE.707 row: H column: 9
Plate: RE.707 row: H column: 9
High quality sequence stop: 599.
Location/Qualifiers
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                                                                                                                                                                                             BDGP/HHMI RE Drosophila EST Project Unpublished (2001)
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                                                                                                                                                                                                                                                Contact: Stapleton, M.
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Contact: Stapleton, M.
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KEYWORDS
SOURCE
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AUTHORS
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BI363229
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Inote="Organ: embryo; Vector: pFlc1; Site_1: Xho1; Site_2: BamHI; Library was Kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library.
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BISTO4-Sprime RE Drosophila melanogaster normalized Embryo pFlc-1
Drosophila melanogaster cDNA clone REL5004 5 similar to
BG:DS01219.1: PBan0004482 located on: 2L 35B9-35B9;: 04/12/2001,
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Budydroidea, Endopterygota, Diptera, Brachycera, Muscomorpha,
1 (bases 1 to 641)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Garlson, J., Champe, M., Chavez, C., Dorsett, V., Parfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
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/clone lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
Disc. 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

Est. 510 486 6798

Est. 510 486 
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One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003645: arm:2L [14622887,14883853]
estimated-cyto:3585-3589: 04/12/2001
Plate: RE.150 row: A column: 4
High quality sequence stop: 604.
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/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE47990"
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95.0%; Pred. No. 1.5e+02;
cive 0; Mismatches 1;
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Matches 19; Conservative
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/note="end : TET3"
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                                         2 ATAACGCAAATAACGCTACG 21
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19; Conservative
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Matches 17; Conserv
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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CNS0014B/c
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TITLE
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                                                                                                        Inote="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was Kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotta, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Eukaryotta, Metazoa, Arthropoda, Brachycera; Muscomorpha,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
1 (bases 1 to 674)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B.,
Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
Pholanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
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/lab_host="DH5-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003645: arm:2L [14622887,14883853]
estimated-cyto:3585-3589: 05/12/2001
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                                                                                                                                                                                                                                               Score 18.4; DB 4; Length 641; Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                           0; Mismatches
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High quality sequence stop: 634.
Location/Qualifiers
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                              272 ATAACGCAAATAACGATACG 291
                                                                                                                                                                                                                                                                                                                                       2 ATAACGCAAATAACGCTACG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="RE24843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI231884.1 GI:14699148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                               76.7%;
95.0%;
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pFlc-1"
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubin, G.M.
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LOCUS DEFINITION

RESULT 7 BI231884

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ORIGIN

ORGANISM

AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

FEATURES

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Useroscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 RYNX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
       DNA linear GSS 04-JUN-1999 survey sequence TET3 end of BAC #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR03F05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE225571

MD0480 Meloidogyne incognita J2 (#MD99-1) Meloidogyne incognita CDNA clone 3292 5' similar to putative importin alpha subunit (Q19969), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meloidogyne incognita (southern root-knot nematode)
Meloidogyne incognita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4; DB 9;
Pred. No. 1.6e+02;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Gapa

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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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/db_xref="texon7159"
/clone="NDL.13d3"
/clone_lib="Notre Dame Liverpool"
/note="voctor: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio genomic clone DKEY-6M14, genomic survey sequence.
AL737121
AL737121.1 GI:21353726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humphray, S.J., Huckle, E. and Hunt, S.E. Direct Submission Submitsed (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 6M14. 6M14 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Cyptiniformes, Cyptinidae, Danio.
(bases 1 to 617)
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                     ch 75.8%; Score 18.2; DB 8; Length 731; 1 Similarity 87.0%; Pred. No. 1.9e+02; 20; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
     /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-6M14"
                                                                                                                                                                                                                                                                                                                                                                                                                       |||| ||||| ||||| ||||| |||| |||||| 691
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Danio rerio
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CNS005B0/c
                                                                                                                                                                                                                                                                                                                                            Matches
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDL.13J3.T7 Notre Dame Liverpool Aedes aegypti genomic clone NDL.13J3, genomic survey sequence. CC111452 GC111452. GC159980507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="second stage preparasitic juveniles (J2)"
/clone_lib="Meloidogyne incognita J2 (#MD99-1)"
/clone_lbe="Meloidogyne incognita J2 (#MD99-1)"
/note="Vector: pNRAI, Site_1: Sfi IA; Site_2: Sfi IB; CDNA was synthesized using 'SNRAF II oligo. CDS_III oligo
d(T)30 (Clontech) and Superscript II reverse
transcriptase (Life Technology). CDNA clones were size fractionated and directionally ligated in the Sfi IA restriction site at 5' end and Sfi IB at 3' end of pMAKI. pMAKI was derived from the plasmid pcDNA II (Invitrogen)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                            Contact: Smart G / Dautova M
Laboratory of Nematology
Mageningen University and Research Center
Box 8123, Binnenhaven 10, 6709 PD Wageningen, The Netherlands
Tel: 31 317 484 254
Exa: 31 317 484 254
Email: Geert.SmantGemedew.nema.wau.nl,
Makedonka.Dautova@medew.nema.wau.nl
Insert.Length: 488 Std Error: 0.00
Seq primer: T7 promoter primer
High quality sequence stop: 488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Tylenchoidea; Heteroderidae, Meloidogyninae, Meloidogyne.
1 (bases 1 to 488)
Dautova,M., Gommers,F.J., Bakker,J. and Smant,G.
5' end expressed sequence tags from Meloidogyne incognita preparasitic J2 cNM library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 75.8%; Score 18.2; DB 2; Length 488; I Similarity 87.0%; Pred. No. 1.9e+02; 20; Conservative 0; Mismatches 3; Indels
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1 (basea 1 to 731)
Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other 2658: NDL.131.SP6
Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Meloidogyne incognita"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library wrs provided by David Severson
Seg primer: 77
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:6306"
/clone="3292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CATAACGCAAATAACGCTACGCA 23
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Matches 20; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

ACCESSION

RESULT 10 CC111452 LOCUS

ORIGIN

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Gaps

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EST 30-AUG-2004

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

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/tissue type="whole placenta, 2 pooled"
/tissue type="whole placenta, 2 pooled"
/lab host="while Tona"
/clone_lib="NIH MGC_270"
/note="Organ: placenta; Vector: pExpress-1; Site_l: EcoRV;
Site_2: Not1; Tissue was collected from two pooled
placentas from the 21st day of pregnancy. 1st strand cDNA
was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was cloned into the Not I and EcoRV
sites of pExpress-1. Library was size-selected for >1.25
kb fragments for an average insert size of 2.15 kb.
Library was normalized to Cot7. A non-normalized version
of this library is also available (NIH MGC_269). Library
was constructed by Open Biosystems (Huntsville, AL). Note:
this is a Mammalian Gene Collection library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outlantshed (1994)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical
College of Wisconsin: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencurt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the 1.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LiAM15747 row: k column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 646)
NIH-MC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CV105677 646 bp mRNA linear EST 30-A
AGENCOURT 31544838 NIH MGC_270 Rattus norvegicus cDNA clone
IMAGE:7445806 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                     or fish"
                                                                                                                                                                                                                                                                                                                                            Query Match 73.3%; Score 17.6; DB 1; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 20; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .646
/organism="Rattus norvegicus"
                                                   /mol type="mkNA"
/strain="local wildtype"
/db_xref="taxon:7955"
/clone="153-C11-2"
/tissue type="whole embryo or
/dev_stage="mixed stages"
/clone_lib="PQR-Z1+Z2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 400.
Location/Qualifiers
      1. .533
/organism="Danio rerio"
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/db_xref="taxon:10116"
/clone="IMAGE:7445806"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 CATAGAGCAAATAACGCTGCACAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CATAACGCAAATAACGCTACGCAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV105677.1 GI:51613733
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CV105677/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                         He just sludge that can be the standard of the standard of the standard of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, no bw sp., the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL915262 AL-Z1+Z2 Danio rerio cDNA clone 153-C11-2, mRNA sequence. AL915262
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                                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cyprinidae; Danio.

(Cyprinicomes; Cyprinidae; Danio.

(Cases 1 to 53)

Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Mang,W., Wen,Z. and Peng,J.

1500 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.2%; Score 17.8; DB 9; Length 923; 90.5%; Pred. No. 3.1e+02; ive 0; Mismatches 2; Indels C
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Lab of Functional Genomics
Institute of Molecular and Cell Biology
Medical Drive, Singapore, 117609, Singapore
Email: pengir@incb.a-star.edu.sg
Clone_requests: info@openbiosystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
| Da_xref="taxon:7227"
| Clone="BACR11022"
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6705 Odyssey Drive, Huntsville, AL 35806.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 13 (3), 455-466 (2003) 22505427
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Danio rerio
                                                                                                  (bases 1 to 923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                               Direct Submission
                                                                                                                                  Зеповсоре
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DEFINITION ACCESSION VERSION

KEYWORDS SOURCE ORGANISM

JOURNAL MEDLINE PUBMED

COMMENT

AUTHORS REFERENCE

TITLE

FEATURES

RESULT 13 AL915262/c

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source

ORIGIN

FEATURES

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 671)

S Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J. and Wing, R. and Wing, R. Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J. and Wing, R. and Wing and Wing and Wing and Wing and Wing and Wing Arizona Genomics Institute
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                ZMWBBb0342E06.f ZMWBBb Zea mays genomic clone ZMMBBb0342E06 5', genomic survey sequence.
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                                        ô
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="DH108"
/clone lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Query Match
Pest Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%; Score 17.6; DB 9; Length 671; Best Local Similarity 83.3%; Pred. No. 3.9e+02; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: M13r
Plate: 0342 row: B column: 06
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4577"
clone="ZMMBBb0342E06"
                                                                                               317 CATAATGCAAATTACCCTACGTAT 294
                                                                             1 CATAACGCAAATAACGCTACGCAT 24
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                                                                                                                                                                                                                                                                                            CG796914.1 GI:38215301
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Zea mays
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CG796914/c
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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Search completed: April 24, 2005, 05:28:28 Job time : 1274.32 secs

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28743, A 287444, A 287444, A 223981, A 23394, A 23394, A 233981, A 23981, A 37981, A 40621, A 40621, A 40621, A 40621, A 40621, A

Sequence Sequence Sequence Sequence

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Sequence

Sequence

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Sequence 4 Sequence 3 Sequence 3

Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence 12779, Sequence 12780, Sequence 12780, Sequence 12780, Sequence 37981,

Sequence Sequence Sequence Sequence Sequence Sequence

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US-08-831-310-18
Sequence 18, Application US/0831310
Feducation No. US20020026035A1
FORDIcation No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
US-10-363-345A-28743

US-10-363-345A-28744

US-10-363-483A-28744

US-10-363-483A-28744

US-10-363-485A-12739

US-10-363-345A-12780

US-10-363-345A-12780

US-10-363-345A-12780

US-10-363-345A-12780

US-10-363-345A-37981

US-10-363-345A-37981

US-10-363-345A-37981

US-10-363-345A-8061

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US-10-363-345A-8061

US-10-363-345A-40021

US-10-363-345A-35875

US-10-363-345A-35875

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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06132/037001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Clark & Elbing LLP
STREET: 176 Pederal Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REPRENCE/DOCKET NUMBER: 0613:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY.

ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TOWNTER: IBM Compatible
TOWNTER: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: U
                                                                                                                                                                                                                                                                                                            Sequence 18, Appl
Sequence 243, Appl
Sequence 243, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 481, Appl
Sequence 39463, Appl
Sequence 39463, Appl
Sequence 39463, Appli
                                                                                                                                                   April 24, 2005, 02:04:39 ; Search time 194.028 Seconds (without alignments) 750.949 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-881-752A-243
US-08-811-310-1
US-10-039-183A-1
7 US-10-335-977-483
B US-10-353-345A-39464
US-10-363-483A-39464
US-10-363-483A-39464
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                      5633728 segs, 3035525691 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-831-310-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Result

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Sequence 1, Application US/08831310
; Fublication No. US20020026035A1
; Fublication No. US20020026035A1
; Fublication No. US20020026035A1
; Fublication No. US20020026035A1
; TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
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                                                                                                                                            Query Match
100.0%; Score 24; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 24; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR.1997
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                 123 CATAACGCAAATAACGCTACGCAT 146
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LOCATION: 106...1002;
CTHER INFORMATION:
NAME/KEY: Signal Sequence;
LOCATION: 106...166;
CYTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
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Best Local Similarity 100.(
Matches 24; Conservative
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TELEX:
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                                                ; NAME/KEY: CDS
; LOCATION: (51)...(947)
US-09-881-752A-243
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                  US-08-831-310-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Al-Garawi, Amal APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles APPLICANT: Miller, Charles APPLICANT: Tomb, Jean-Francis APPLICANT: Tomb, Jean-Francis APPLICANT: Tomb, Jean-Francis APPLICANT: Oomen, Raymond P. TITLE OF INVENTION: Encoding No. US20020115078Alel Helicobacter Polypeptides in the TITLE OF INVENTION: Genome FILE REFERENCE: 06132/041002 CURRENT APPLICATION NUMBER: US/09/881,752A CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: US 08/833,457 PRIOR APPLICATION NUMBER: US 08/833,457 NUMBER OF SEQ ID NOS: 370 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 243 LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lissolo, Ling
APPLICANT: Tissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Thile or Invention: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REFERENCE: 06132/037003.183A
CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                         Score 24; DB 8; Length 24; Pred. No. 0.41;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                      Query Match
100.0%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.4
Matches 24; Conservative 0; Mismatches
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Patent No. US20020115078A1
PAPERAL INFORMATION:
APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/10039183A Publication No. US20030143242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kleanthous, Harold APPLICANT: Lissolo, Ling
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                         LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-881-752A-243
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US-10-039-183A-18
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
TELEPHONE:
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                       Sequence 1, Application US/10039183A
| Sequence 1, Application US/2003143242A1
| Publication No. US20030143242A1
| Publication No. US20030143242A1
| GENERAL INFORMATION:
| APPLICANT: Kleanthous, Harold
| APPLICANT: Lissolo, Ling
| APPLICANT: Millar, Charles
| TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
| TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
| TITLE OF INVENTION: NUMBER: US/10/039,183A
| CURRENT FILING DATE: 1997-04-01
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 1
| LENGTH: 1149
| TYPE: DAR
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Sequence 481, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH ET AL
ATILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 24; DB 15; Length 1149; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 24; Conservative 0; Mismatches 0; Indels 0
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
NAME: Mandragouras, Augustration NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (106)...(1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: sig_peptide
; LOCATION: (106)...(166)
US-10-039-183A-1
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Publication No. US20040052799A1
GENERAL INPORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et AL
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.0%; Score 19.2; DB 17;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATE: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...456
; SEQUENCE DESCRIPTION: SEQ ID NO: 481:
US-10-335-977-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CATAATGCGAATAACTCTACGCAT 111
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                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 481:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 30464, Application US/10363483A

| Sequence 30464, Application US/10363483A
| Publication No. US20050064401A1
| GENERAL INFORMATION:
| APPLICAMT: Alexander Olek
| APPLICAMT: Christian Plepenbrock
| APPLICAMT: Kurt Berlin
| TITLE OF INVENTION: 11 nesses
| TITLE OF INVENTION: 11 nesses
| FILE REFERENCE: 82011
| CURRENT APPLICATION NUMBER: US/10/363,483A
| CURRENT FILING DATE: 2003-03-03
| NUMBER OF SEQ ID NOS: 40712
| SEQ ID NO 39464
| LENGTH: 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: unsure
; LOCATION: (883, 910, 912, 922..923, 925, 931..932, 934, 939..940, 949..)
US-10-363-483A-39463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain

TITLE OF INVENTION: Illnesses

FILE REFERENCE: 82011

CURRENT APPLICATION NUMBER: US/10/363,483A

CURRENT FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 39463
          LOCATION: (124..125, 135..136, 141..142, 144, 150..151, 153, 163, 165)
FEATURE:
                                                                                                                                                                                                                               Gaps
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FEATURE:
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                                                                                                                                                                          76.7%; Score 18.4; DB 18; Length 1074; 95.0%; Pred. No. 2e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 39463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.7%; Score 18.4; DB 19; Best Local Similarity 95.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 1;
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; Sequence 39463, Application US/10363483A
; Publication No. US20050064401A1
                                                                                                                                                                                                                                                                                                           200 TAACGCGAATAACGCTACGC 219
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                   Query Match
Best Local Similarity 95.0°
Matches 19, Conservative
                                                                       NAME/KEY: unsure
                                                                                                   ; LOCATION: (192)
US-10-363-345A-39464
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US-10-363-345A-39464

US-10-363-345A-39464

Sequence 3464, Application US/10363345A

Publication No. US20040234960A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Gytosines in genomic DNA in the sequence context of 5'-CpG-3

FILER REFERENCE: E01/1227

CURRENT APPLICATION NUMBER: US/10/363,345A

CURRENT APPLICATION NUMBER: US/10/363,345A

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 39464
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39463, Application US/10363345A
Sequence 39463, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander ole
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Oytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
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; LOCATION: (883, 910, 912, 922..923, 925, 931..932, 934, 939..940, 949..)
US-10-363-345A-39463
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 39463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.7%; Score 18.4; DB 18; Length 1074; Best Local Similarity 95.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                             Length 900;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                          Match 80.0%; Score 19.2; DB 17; Local Similarity 87.5%; Pred. No. 85; es 21; Conservative 0; Mismatches 3;
                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...900
SEQUENCE DESCRIPTION: SEQ ID NO: 483:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                           73 CATAATGCGAATAACTCTACGCAT 96
                                                                                                                                                                                                                                                                              1 CATAACGCAAATAACGCTACGCAT 24
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ORGANISM: Artificial Sequence
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US-10-363-345A-39463/c
                                                                                                                         US-10-335-977-483
                       FEATURE
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Sequence 28744, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Plepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: illnesses
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28744
; LENGTH: 996
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 20743
LENGTH: 996
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       Gapa
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US-10-363-483A-28744
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     Mismatches
                                                                                                                                                                        RESULT 14
US-10-363-483A-28743/c
; Sequence 28743, Application US/10363483A
; Publication No. US20050064401A1
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                                                   5 ACGCAAATAACGCTACGC 22
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       18; Conservative
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Sequence 28744, Application US/10363345A.

Sublication No. US20040234960A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kut Berlin

TITLE OF INVENTION: Exposines in genomic DNA in the sequence context of 5'-CpG-3

TITLE OF INVENTION: US/10/363,345A

CURRENT APPLICATION NUMBER: US/10/363,345A

CURRENT PILING DATE: 2003-03

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 28744

LENGTH: 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/127
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
SEQ ID NOS: 40712
LENGTH: 996
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NAME/KEY: ungure
LOCATION: (124..125, 135..136, 141..142, 144, 150..151, 153, 163, 165)
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US-10-363-345A-28744
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APPLICANT: Alexander Olek
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; NAME/KEY: ungure
; LOCATION: (192)
US-10-363-483A-39464
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US-10-363-345A-28744
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Sequence 2563, App
Sequence 1350, App
Sequence 12360, A
Sequence 1256, Ap
Sequence 2455, Ap
Sequence 2578, Ap
Sequence 17737, A
Sequence 12871, A
Sequence 12871, A
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Sequence 315, App
Sequence 39, Appl
Sequence 203369,
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Sequence 102, App
Sequence 2563, Ap
Sequence 395, App
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                                                                                                        April 24, 2005, 00:51:24; Search time 46.6479 Seconds (without alignments) 841.853 Million cell updates/sec
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Sequence 1,
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Sequence 2
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                            Run on:
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No.
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Sequence 315, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 315
                                       Sequence 44723, A Sequence 1, Appl.1 Sequence 1, Appl.1 Sequence 52, Appl. Sequence 50, Appl. Sequence 54, Appl. Sequence 54, Appl. Sequence 54, Appl. Sequence 555, Appl. Sequence 555, Appl. Sequence 555, Appl.
                                                                                                                                                                                         Sequence 66, Appl
Sequence 12021, A
Sequence 13021, A
Sequence 16938, A
                                                                                                                                                                                            App]
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                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09336115C

Patent No. 6576244

GENERAL INPORMATION:
APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
TITLE OF INVENTION: Methods Against Helicobacter Infection
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06123/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 4; Length 1149; 100.0%; Pred. No. 0.023; 1ve 0; Mismatches 0; Indels
US-09-634-238-96
US-09-134-001C-774
US-09-949-036A-5236
US-09-949-016-44723
US-08-252-492-1
US-08-27-126-1
US-08-27-61-1
US-09-206-942-50
US-09-206-942-56
US-09-206-942-56
US-09-206-942-56
US-09-206-942-56
US-09-206-942-56
US-09-710-279-4137
US-09-710-279-4137
US-09-710-279-4137
US-09-910-11E-66
US-09-949-016-12021
US-09-949-016-12021
US-09-949-016-13021
                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATAACGCAAATAACGCTACGCAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 24; Conservative
 FEATURE: NAME/KEY: CDS LOCATION: (106)...(1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: 81g peptide
LOCATION: (106)...(166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-540-236-315/c
                                                                                                                                                                                                                                                                                                                             US-09-336-115C-23
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ORGANISM: Human
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                     Query Match
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i Sequence 203369, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FBALSEQ for Windows Version 4.0

LENGTH: 601

LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lagace, Robert, E.

APPLICANT: Barg, Kim, L.

APPLICANT: Berg, Kim, L.

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME

FILE REPERENCE: PM-0008-4 US

CURRENT APPLICATION NUMBER: US/09/596,002

CURRENT FILING DATE: 2000-6-16

FRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS:

SOFTWARE PELL PROGram

SEQ ID NO 39

LENGTH: 10848

TYPE: DNA

ORGANISM: M. catarrhalis

FRAUTHER.
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                                                                                                 Score 16.8; DB 4; Length 1209;
Pred. No. 80;
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                                                                                                                                                 Indels
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; OTHER INFORMATION: Incyte template ID No. 6632636 39
; PUBLICATION INFORMATION:
US-09-596-002-39
                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 4;
Pred. No. 1.6e+02;
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                               RESULT 3
US-09-596-002-39/c
; Sequence 39, Application US/09596002
; Patent No. 6632636
                                                                                                                                                                                                                                 935 CATAACGCAAATAATGCTTC 916
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                                                                                                     Query Match 70.0%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-315
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; ORGANISM: Human
US-09-949-016-203369
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RESULT 5

US-09-949-016-17482/C

Sequence 17482, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-30

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FASTSEQ FOR Windows Version 4.0

SEQ ID NO 17482
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                                                Gaps
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Burland, Valerie
Perna, Micole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
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Length 601;
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ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
    DB 4;
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                                             0; Mismatches
Score 16.6;
Pred. No. 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13226 CATAACCCAGATAACTCTACTCA 13204
                                                                                                                                        557 CATAACCCAGATAACTCTACTCA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-453-702B-102/c
; Sequence 102, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
                                                                                             1 CATAACGCAAATAACGCTACGCA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CATAACGCAAATAACGCTACGCA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(76962)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17482
69.2%;
                                                19; Conservative
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                          Best Local Similarity
Matches 19; Conserv
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Gaps
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APPLICANT: Schroder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: CORYNEASCHRIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
CURRENT APPLICATION NUMBER: US/09/602,777A
PRIOR APPLICATION NUMBER: US/09/602,777A
PRIOR APPLICATION NUMBER: US/09/602,777A
PRIOR APPLICATION NUMBER: US/09/602,777A
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                                                                                                                                                                                              NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1569
; SEQUENCE DESCRIPTION: SEQ ID NO: 2563:
US-09-107-532A-2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PELICATION NUMBER: DE 19932128.0
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR PILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: DE 1993292.2
PRIOR PELICATION NUMBER: DE 1993292.2
PRIOR PELICATION NUMBER: DE 1993292.4
PRIOR PELICATION NUMBER: DE 1993293.3
PRIOR PELICATION NUMBER: DE 1993293.3
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: DE 1993293.3
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: DE 1993293.3
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: DE 1993293.4
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: DE 1993293.7
PRIOR APPLICATION NUMBER: DE 1993293.7
TOPOLOGY: circular
MOLECULE TYPE: DNA.(genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: DE 19933003.4
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-602-777A-395/c
; Sequence 395, Application US/09602777A
; Patent No. 6831165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 AACTCAACTAACGATACGCAT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AACGCAAATAACGCTACGCAT 24
                                                                                                                                                                                       FEATURE
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                 NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOWMUNICATION INPORMATION:
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 7886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: JA MAY 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: JA MAY 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: JA MAY 1998
APPLICATION NUMBER: 60/081571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-453-7028-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION:
TELEPHONE: (781) 893-5007
                                                                                                                         APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                    FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1083 CATAACGCAATTAACGCT 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1569 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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Application US/09949016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2455
LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Sequence 13304, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ for Windows Version 4.0
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85.7%; Pred. No. 3.1e+02;
tive 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.5%; Score 16.2; DB 4; Length 1977; Best Local Similarity 85.7%; Pred. No. 1.7e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0
PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933006.9

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR PLING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                887 AACGCAAAGAACGCAACCCAT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AACGCAAATAACGCTACGCAT 24
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; LOCATION: (1)...(120213)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (101)..(1954)
; OTHER INFORMATION: RXN02508
US-09-602-777A-395
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Best Local Similarity 85.7
Matches 18; Conservative
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US-09-949-016-13304/c
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LENGTH: 120213
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RESULT 10 US-09-949-016-12260/c

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JAPPLICATION STATISTICAL APPLICATION AND USES THEREOF TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO130: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOO14-14

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

SERIOR PLING DATE: 2000-10-03
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Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 03/09/270,767
CURRENT FILING DATE: 1999-03-17
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10-09-270-767-17737/c
| Sequence 17737, Application US/09270767
| Patent No. 6703491
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| LOCATION: (1)...(120217)
| CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12260
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; ORGANISM: Drosophila melanogaster
US-09-270-767-2455
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Best Local Similarity 79.2%;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-3

PRIOR PILING DATE: 2000-10-3

PRIOR PILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING
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       Length 100836;
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       Score 16; DB 4; I
Pred. No. 3.8e+02;
0; Mismatches 5
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; Sequence 17063, Application US/09949016
; Patent No. 6812339
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17063
66.7%;
nilarity 79.2%; Conservative 0;
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       Query Match
Best Local Similarity
Matches 19; Conserv
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APPLICANT: Gary L. Brecon et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2578
LENGTH: 1023
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-09-08
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Pred. No. 1.5e+02;
0; Mismatches 5; Indels
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illarity 79.2%; Pred. No. 1.9e+02;
Conservative 0; Mismarch--
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6562958
                                                                                                                                        ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17737
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US-09-949-016-12871
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-2578
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
   NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17737
LENGTH: 169
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Best Local Similarity
Matches 19; Conserv
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US-09-328-352-2578/c
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Title: Perfect score:

Sequence:

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Scoring table;

Searched:

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gastritis; ulcer; vaccine; diagnosis; therapy; PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
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                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                           AAZ01425
ABQ53430
ABQ53431
ABQ49284
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ADA20368
ADA84175
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97US-00834666.
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                                                                                                                                                                                                                                                                                                                                                            AAV07973 standard; DNA; 24
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(first entry)
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Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1997;
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02-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer; 88.
           AAV07973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-)
                                                                                                                                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                                                                                                                                                  AAV07973
                                                                                                                                                                                                                                                                                                                                                              Aav90591 Nucleotid
Aav90580 Nucleotid
Aav24659 H. pylori
Abq52872 Oligonucl
Abq42152 Oligonucl
Abq42152 Oligonucl
Abq42153 Oligonucl
Abl34421 Human imm
Abd26189 Oligonucl
Abq26189 Oligonucl
Abq26189 Oligonucl
Abq21390 Oligonucl
Abq51391 Oligonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aad61576 Helicobac
Aav90844 Nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aav07973 Helicobac
                                                                 April 23, 2005, 10:03:10 ; Search time 157.69 Seconds (without alignments) 900.968 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                      8780412
5.1.6
Compugen Ltd.
                                                                                                                                                                                              4390206 segs, 2959870667 residues
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
 GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX14041
AAV07963
AAD61576
AAV90844
                                             nucleic search, using sw model
                                                                                                                                       cataacgcaaataacgctacgcat
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AAV24859
ABQ52872
ABQ52873
ABQ42153
ABC42153
ABL34401
ABL346188
ABQ26188
ABQ26188
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Gapop 10.0 , Gapext 1.0
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geneseqn2004bs:*
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seq length: 200000000
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44 111 112 113 114 116 116 117 118 118

Score

Result

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AAVO7963

AAVO7964

AAVO79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections.
also used with a different 5' primer (see AAV07970) to ampligy DNA encoding mature GPHO 1360. The isolated polymelectides, and encoded polypeptides, can be used to develop vaccines for the treatment and prevention of Helicobacter infection. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Helicobacter infection; gastroduodenal disease; gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1000 BP; 372 A; 167 C; 207 G; 254 T; 0 U; 0 Other;
                                                                                                                                                            Score 24; DB 2; Length 24; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oomen RP;
                                                                                                                                                                                                     0; Indels
                                                                                                                       Sequence 24 BP; 10 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Al-Garawi A, Miller C,
                                                                                                                                                                                                                                        1 CATAACGCAAATAACGCTACGCAT 24
                                                                                                                                                                                                                                                                                 CATAACGCAAATAACGCTACGCAT 24
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51. .950
/*tag= a
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                                                                                                                                                          ch 100.0%; cl Similarity 100.0%; 24; Conservative 0.
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97US-00902615.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptic ulcer disease, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori GHPO 1360 gene
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
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                                                                                PI field.)
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This DNA sequence codes for a 32 kDa Helicobacter pylori polypeptide (see AAW73034) designated GHPO 1360. A polynucleotide encoding the unprocessed, or the mature, GHPO 1360 can be obtained from genomic DNA by CR CR amplification (see AAW70969-70 and AAW07973). The invention provides polynucleotides (see AAW72001, AAW07912-21 and AAW07963-64) encoding a can a 50 kDa Helicobacter polypeptide (see AAW73055). These polynucleotides were initially identified in a search of H. pylori genomic databases. DNA cassettes for expression of the Helicobacter proteins (unprocessed or mature forms) in prokaryotic or euksaryotic cells are provided. The polynucleotides can be used in vacciness to prevent or treat Hb infection of Products and methods of the invention allow treatment and prevention of gastroducdenal diseases associated with Hb infections, including acute, cronnic, and arrophic gastriic and detection methods are also provided. Cand ducdenal ulcers. Diagnostic and detection methods are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHPO 1360; infection; gastritis; ulcer; vaccine; diagnosis; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori 32 kDa polypeptide GHPO 1360 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 148-149; 184pp; English.
                                       123 CATAACGCAAATAACGCTACGCAT 146
24
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1 CATAACGCAAATAACGCTACGCAT
                                                                                                                                                                                                                         AAV07963 standard; DNA; 1149
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106. .166
/*tag= b
167. .1002
/*tag= c
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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02-FEB-1999
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Sequence 1149 BP; 412 A; 185 C; 242 G; 310 T; 0 U; 0 Other;

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178 CATAACGCAAATAACGCTACGCAT 201

BP

(first entry)

24

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Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                            (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                           Nucleotide sequence of cluster 3.
                                                                              AAV90844 standard; DNA; 1082
                                                                                                                                                                                                                 Helicobacter pylori
                                                                                                                                                                                                                                                                                      25-APR-1998;
                                                                                                                                                                                                                                         WO9849314-A2
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                                                                                                    AAV90844;
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AAV90591
                                                                   AAV90844
ID AAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for inducing protective immune response to Helicobacter infection. The method comprising administering to a mammal by injection an immunogenic Helicobacter pylori bolypeptide comprising a subunit of H.pylori urease admixed with an adjuvant having one or more heat-liable toxin of Escherichia coli (LT), B subunit of LT (LTB), cholera toxin (CT), and B subunit of CT. The method is useful for inducing an immune response to Helicobacter infection in a mammal. The method is useful for both treatment and prevention of H.pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing immune response to Helicobacter useful for treating Helicobacter pylori infection, by administering immunogenic Helicobacter polypeptide admixed with adjuvant having heat-liable toxin of Escherichia coli.
                                                                                                                                                                                                                Immune response; Helicobacter infection; adjuvant; heat-liable toxin; LT; cholera toxin; CT; urease; therapy; antibacterial; vaccine; antigen; p32;
                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 24; DB 10; Length 1149; 1 Similarity 100:0%; Pred. No. 0.21; 24; Conservative 0; Mismatches 0; Indels 0.
 2; Length 1149;
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                      0; Indels
DB 2;
Match 100.0%; Score 24; DE Local Similarity 100.0%; Pred. No. 0.2 (68 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                    product= "Antigen p32"
                                                                                                                                                                                                                                                                                                                                            /*tag= b
167. .1002
/*tag= c
/product= "Mature p32"
                                                           178 CATAACGCAAATAACGCTACGCAT 201
                                            24
                                                                                                                                                                                            Helicobacter pylori p32 antigen DNA
                                                                                                                                                                                                                                                                                     Location/Qualifiers
106. .1005
/*tag= a
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                                            1 CATAACGCAAATAACGCTACGCAT
                                                                                                                        AAD61576 standard; DNA; 1149
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Best Local Similarity
Matches 24; Conserv
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Query Match
                      Matches
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98WO-US008487. 97US-0045107P.

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                                                                                                                                                  New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                             Claim 20, Page 281-282; 402pp; English.
Chow TP, Fry KE, Lim MY, Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 CATAACGCAGATAACGCTACGCAT 260
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Les 23, Conservative
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                                                                             WPI; 1999-009433/01.
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Gaps

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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and appecific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm exadication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                        New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1117 BP; 388 A; 202 C; 234 G; 293 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%; Score 22.4; DB 2; 95.8%; Pred. No. 1.1; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "no stop codon given"
                                                                                                                                         Lim MY, Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 CATAACGCAGATAACGCTACGCAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATAACGCAAATAACGCTACGCAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Claim 27; Page 119; 402pp; English.
                                                                                                 (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV24638 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00625811.
96US-00758731.
96US-00736905.
96US-00738859.
98WO-US008487.
                                        97US-0045107P
                                                           97US-0061958P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori ORF 03xe11215orf7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                    WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                           Chow TP, Pry KE,
                                                                                                                                                                                                       P-PSDB; AAW89829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterium; ds
  25-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
                                        25-APR-1997;
                                                           14-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is characterised by immunoreactivity with H. Pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a Helicobacter pylori antigenic protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%; Score 22.4; DB 2; Length 1082; 95.8%; Pred. No. 1.1; 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1082 BP; 383 A; 189 C; 222 G; 288 T; D U; O Other;
                                          Nucleotide sequence of clone Y104.1.ASM from cluster 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence from clone Y104-1.asm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page 123-124; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 CATAACGCAGATAACGCTACGCAT 260
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                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENELABS TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                        97US-0045107P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lasting immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
                                                                                                                                           Helicobacter pylori
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                                                                                                                                                                                    WO9849314-A2
                                                                                                                                                                                                                                                                  25-APR-1998;
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    18-FEB-1999
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18-FEB-1999
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Chow TP,

AAV90580;

RESULT 7 AAV90580

Query Match Best Loca Matches

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01-SEP-2001; 2001WO-EP010074.
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                                                                                                                                                                                   Smith D, Alm RA;
                                                                                                                                        (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                        P-PSDB; AAWS5450
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29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
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                                                                                          06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                    Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic, vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.2; DB 2; Length 456; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 456 BP; 170 A; 79 C; 106 G; 101 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori cell envelope OMP ORF 02ae11612_22477267_f2_27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Э,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATAATGCGAATAACTCTACGCAT 111
                                                                                                                                                                                                                                                                                               Claim 5,6; Page 155; 1145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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96US-00761318
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1 Similarity 87.5%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                   WPI; 1997-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                          Alm RA;
                                           (ASTR ) ASTRA AB.
                                                                                                                                                           P-PSDB; AAW55229
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9737044-A1
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                                                                                        Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV24859;
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This sequence encodes a H. pylori cell envelope outer membrane protein (OMP) having no terminal Phe residue. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori of H. pylori specific antigens. The genomic sequence of H. pylori of TATC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial C. C. the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ONR were analysed for significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 39463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5,6,21; Page 288; 1145pp; English.
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96US-00625811.
96US-00758731.
96US-00736905.
96US-00738859.
96US-00761318.
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les 21; Conservative
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CgG-3', present in a genomic sample of DNA. The sample is treated chemically to convert genomic sample of DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosts and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation is created and the methylation of cell or the contral and cessive of many C residues to be determined similtaneously, the methylation of cell or the contral and cell differentiation. The method allows the methylation and control of the central 
                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4; DB 6; Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1074 BP; 394 A; 375 C; 114 G; 175 T; 0 U; 16 Other;
                                                                                                                                                                                                                                                                                                                                      Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 81;
0; Mismatches
                                                                                            Guetig
                                                                                         Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 TAACGCGAATAACGCTACGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TAACGCAAATAACGCTACGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ42152 standard; DNA; 996 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-2001; 2001WO-EP010074.
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05-SEP-2000; 2000DE-01044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2002 (first entry)
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                                                                                         Piepenbrock C,
                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                   WPI; 2002-371829/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200218632-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ42152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                         olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
ABQ42152/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic convert of the degree of but not methylated C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation seatus of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method in the for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                         Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.4; DB 6; Length 1074;
Pred. No. 81;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1074 BP; 175 A; 114 C; 375 G; 394 T; 0 U; 16 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                      Guetig D;
                                                                                                                                                                                   Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           875 TAACGCGAATAACGCTACGC 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ52873 standard; DNA; 1074 BP
                         01-SEP-2000; 2000DE-01043826.
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Local Similarity 95.0%;
les 19; Conservative (
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05-SEP-2000; 2000DE-01044543.
                                                                                                                                                                                                                                                                                                                                            diagnosis and prognosis, com
from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disclosure of the invention
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                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                         (EPIG-) EPIGENOMICS AG.
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                                            Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif S'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:
                                                                                                                                                                                                                                                                                                                     and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nuclectide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation statum of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for detecting cytosine methylation SEQ ID NO 28744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 18; DB 6; Length 996; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 996 BP; 130 A; 113 C; 352 G; 401 T; 0 U; 0 Other;
                                                                                                                        German
 Guetig D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guetig D;
                                                                                                                      Claim 12; 56pp + Sequence Listing; 56pp;
Berlin K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 ACGCAAATAACGCTACGC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-01043826, 05-SEP-2000; 2000DE-01044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match , 75.0
Best Local Similarity 100.
Matches 18; Conservative
Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                              WPI; 2002-371829/40.
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Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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methylation of a particular account methylation of a particular amover methylation of a particular cytosine in a motif 5'-cp6'-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligometolecides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of clip amplicon. From the ratio of labels hybridised to the two classes of clip amplicon. From the ratio of labels hybridised to the central clip for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervolus cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP'S); and (ii) for differentiation. The method allows the methylation investigating cell differentiation. The method allows the methylation actual carbus of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for the determining the degree of cytosine methylation described in the
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of cytosine methylation in genomic DNA, useful for s, comprises selective hybridization of amplicons
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                           This invention describes a novel method for determining the degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 6; Length 996
Pred. No. 1.2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 2374.
                                                                                                        Claim 12, 56pp + Sequence Listing, 56pp, German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
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100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ACGCAAATAACGCTACGC 22
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01-SEP-2000; 2000DE-01043826
                            diagnosis and prognosis, com
from chemically treated DNA.
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ABL34401 standard; DNA; 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antianteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; opthhalmological; antirheumatic; antiartitic; antidiabetic; antisoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 719 BP; 116 A; 76 C; 194 G; 333 T; 0 U; 0 Other;
                                                                                                                                                                                                         Claim 1; SEQ ID NO 2374; 32pp + Sequence Listing; German
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01-SEP-2000; 2000DE-01043826
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WPI; 2002-130909/17
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,

Claim 1; SEQ ID NO 2394; 32pp + Sequence Listing; German.

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine

Berlin K;

Olek A, Piepenbrock C,

WPI; 2002-130909/17

methylation

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including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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1.9e+02;
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Search completed: April 24, 2005, 02:20:10 Job time : 159.69 secs

Scoring table:

Minimum DB Maximum DB

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AC12151 Medicago
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G01N3/554, G01N33/569
Strandedness: Single, Topology: Linear: Linear Location/Qualifiers.
 Drosophil
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
Viruses; lto 24)

L (bases 1 to 24)

Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polynucleotide molecules
Astent: 1P 2001529354-A 63 27-NOV-2001;
MERIEUX ORAVAX SOCIETE EN NOW COLLECTIF PASTEUR MERIEUX SERUMS E'
VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC
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HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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/mol_type="genomic DNA"
    /db_xref="taxon:10509"

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AC122161
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AX347323
AB119449
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27-NOV-2001
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BD092341 Ide
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Helicobacter pylori 26695 section 16 of 134 of the complete genome.
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Helicobacter pylori 26695
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Bacteracaes Helicobacter.
1 (bases 1 to 11421)
Tomb,J.-F., White,O., Kertchum,K.A., Klenk,H.P., Gill,S.,
Fleischman,R.D., Ketchum,K.A., Klenk,H.P., Gill,S.,
Dougherty,B.A., Nelson,K., Quackenbush,J., Zhou,L., Kirkness,B.F.,
Peterson,S., Loftus,B., Richardson,D., Dodson,R., Khalak,H.G.,
Glodek,A., McKenney,K., Fitzegerald,L.M., Lee,N., Adams,M.D.,
                                                                                                                                                                                                         BD082346 1149 bp DNA linear PAT 27-AUG-2002 76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
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HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES PI
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A61K39/40,
G01N33/554, G01N33/569
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae.

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Topology: Linear;
Key
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27-NOV-2001
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                                     24; Conservative
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Best Local Similarity
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PI AM
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                                                                                                                                                                                                                                          Synthetic construct

Synthetic construct

Cher sequences:

1 Chases 1 to 1000)

2 I Chases 1 to 1000|

3 Kleanthous, H., Garawi, A.A., Miller, C., Tomb, J.F. and Oomen, R.P.

1 I Chases 1 to 1000|

3 Kleanthous, H., Garawi, A.A., Miller, C., Tomb, J.F. and Oomen, R.P.

1 I Chases 1 to 1000|

3 I chastification of polymucleotides encoding novel helicobacter

2 I chastification of polymucleotides encoding novel helicobacter

3 I chastification of polymucleotides encoding novel helicobacter

4 I patent: JP 2001527393-A 122 25-DEC-2001;

5 MERIEUX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET

5 VACCINS AGROBIOLOGICAL RESOURCES MINISTRY O SA, HUMAN GENOME

8 N JP 2001527393-A/122

8 D 25-DEC-2001

8 D 25-DEC-2001

8 D 1998541947

8 D 1-APR-1997 US 08/933457, 24-JUN-1997 US 08/881227 PR

9 D 1-APR-1997 US 08/902615

9 D 1 TOMB,

PRAYMOND PETER COMEN

PRAYMOND PETER COMEN

PC AD1N43/04, A61K31/70

CC Strandedness: Single;

CC Topology: Linear;

FH Key
                                                                                                                                  DNA linear PAT 27-AUG-2002 encoding novel helicobacter
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I (bases 1 to 1149)
Weltzin,R.A. and Guy,B.
LT and CT in parenteral immunization methods against helicobacter
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/organism="synthetic construct"
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                                                                                                                                  BD092341 1000 bp DNA Identification of polynucleotides encodipolypeptides in the helicobacter genome.
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1.5;
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100.0%; Pred. No. 1.5
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: US 6576244-A 23 10-JUN-2003;
Location/Qualifiers
1. 1149
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 from patent US 6576244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 CATAACGCAAATAACGCTACGCAT 146
   24
                             CATAACGCAAATAACGCTACGCAT 24
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                                                                                                                                                                                                            BD092341.1 GI:22637 JP 2001527393-A/122.
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Best Local Similarity 100.
Matches 24; Conservative
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LAPLGNLAFLKTPRNSAFALGFPVGALLFYWCALSFRYSDFTYLLPLIIVLIALVYGV
LFYLLLYFENPYFRLLSFLGSSFIHPFGFDWLVPDSFPSYSVFRVDKLSLGLVFLACI
ELSTKELKKYRIIGYLLLLGALDFNGFKTSDLKKVGNIELVSTKTPQDLKFDSSYLND
IENNILKEIKLAGAGKQYKLIVPFETAPYPIALENSPFKAKLEDLSDNIAILIGTLRTQG
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HLATMLKPRSCTISLLEHQDIYALNSKKLLEERRLKVGITPGSHYLFKGFSALENLQV
STLAKQEINHSLLEQUGIAHTLKGCVGELSGGQQQRLSIARVLSKKPKIIIADEPTG
NLDTTSANQVISMLQNYITEKEGALVLATHDEHLAFTCSQVYRLEKEVLIKEK"
complement (4843. .6120)
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                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:L77117 PID:1591717 percent identity: 36.25; identified by sequence similarity; putative" /codon start=1 /transT_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="spore coat polysaccharide biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HP0179"
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identified by sequence similarity; putative"
/codon start=1
/transI_table=11
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/db_xref="GI:2313268"
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/codon start=1
/transI_table=11
/product="H. pylori predicted coding region HP0181"
                                                                              'product="translation elongation factor EF-P (efp)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to GB:L42023 SP:P44626 PID:1003497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD07248.1"
/db_xref="GI:2313267"
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/gene="HP0179"
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  similarity; putative"
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/transT_table=
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Direct Submission
L. Submitted (Ge.Aug-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transT_table=11
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HILWKTEDBAAKRIPEELDWRKKGAREVKKGAREVKFOONGGDLGRFOONG
MADDRSKAARALTPGDYKTPPWTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEK
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PID:853765 GB:ML009126 percent identity: 45.96; identified
y sequence similarity; putative"
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figtsegaikymgidmavgmvktmceryphipvalhldhgttfescekavkagptsvm
idashhafbenleltskvvkmahnagvsveablgrlmgiednisvdekdavlvnpkea
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VRKSYLDAGGDLKGSKGVPPEFLQESVKGGINKVNTDTDLRIAFIAEVRKVANEDKSQ
FDLRKFFSPAQLALKOVVKERMKLLGSANKI"
                           and
                                                                           The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to PID:671840 SP:Q46105 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-MAR-1999) The Institute for Genomic Research, 9712
Medical Centra Dr. Rockville, MD 20850, USA
Location/Qualifiers
Hickey, E.K., Berg, D.E., Gocayne, J.D., Utterback, T.R.,
Peterson, J.D., Kelley, J.M., Karp, P.D., Smith, H.O., Fraser, C.M.
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protein_id="AAD07246.1"
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|strain="26695"
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1162. .2085
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246. .1145
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gene="HP0176"
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transl_table=
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23; Conservative
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Best Local Similarity 95.8
Matches 23; Conservative
                                                                                                                                                                        Best Local Similarity
Matches 23; Conserv
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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KEYWORDS
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BD061969
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BD061705
LOCUS
                       FEATURES
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KHLEVGPIVLNKGFPATKTGELSIHALBFHILSKTIYPLPEKKHGLSDIELRYRQPY
LDLIVNPSVKDVFKKRSLIVSSVRKFFEMEGFLEVETPMMHPIPGGANARPFITYHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUDG1716 1082 bp DNA linear PAT 27-AUG-2002 Antigenic composition and method of detection for Helicobacter Pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                           LEVERVIRIAPELYLKRII VGGFRAVFEINRNFRNEGMDHSHNPEFTMIEFYWAYHTY
EDVERVIRIAPELYLLKTINLDSKII YNDMEVDFNOGYS VEYLDALETIOGISKOILEK
EDRLLAYLLEQGIKVEPNLYVEKLLARAFDHFVEHQIINPTFVTQYFIEI SPLARRND
SNPNIADRFELFIAGREIANGFSELNDPLOQLERFRNQVAEKEKGDEBAQYMDEDYVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:J01620 SP:P00477 GB:V00283 PID:146218 PID:41603 percent identity: 53.96; identified by sequence
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1 (bases 1 to 1082)
Chow, T.P., FY,K.E., Lim,M.Y. and Mcatee,C.P.
Antigenic composition and method of detection for Helicobacter Patent: JP 2001517091-A 50 02-0CT-2001;
GENERAS TECHNOLOGIES INC
PN JP 2001517091-A/50
PD 02-0CT-2001
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                                                                                                                                                                                                 /note="similar to GB:M63448 SP:P41258 PID:144208 pe.
identity: 58.63; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="serine hydroxymethyltranaferase (glyA)"
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PD 02-0CT-2001

PR 25-APR-1999 JP 1998547263

PR 25-APR-1997 US 60/045107,14-0CT-1997 US (CC 12N15/31,COYK14/205,COYK16/12,A61K39/106

CC Topology: Linear;
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Pred. No. 1.2;
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8567. .9817
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                                                                                                                                      7062. .8567
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gene="HP0182"
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synthetic construct
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Best Local Similarity
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BD061716
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BD061969 1082 bp DNA linear PAT 27-AUG-2002
Antigenic composition and method of detection for Helicobacter
Pylori.
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JP 2001517091-A/303.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1082)
Chow,T.P., Fry,K.E., Lim,M.Y. and Mcatee,C.P.
Antigenic composition and method of detection for Helicobacter
Patent: JP 2001517091-A 303 02-OCT-2001;
PD 02-OCT-2001
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synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1117)
Antiqenic composition and method of detection for Helicobacter
patent: JP 2001517091-A 39 02-OCT-2001;
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Antigenic composition and method of detection for Helicobacter
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PD 02-CCT-2001

PF 25-APR-1998 UP 1998547263

PR 25-APR-1997 US 60/045107,14-OCT-1997 US

THERESA P CHOW,KIRK E FRY,MOON Y LIM,C P MCATEE PC

C12N15/31,C07K4/205,C07K16/12,A61K39/106

CC Strandedness: Single;

CC Topology: Linear;

FR Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Location/Qualifiers.
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                                                                                                                                                             Score 22.4; DI
Pred. No. 8.5;
                                                                                                                                                                                                   0; Mismatches

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BD061705.1 GI:22607310
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COMPLement (687. .950)
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/note="similar to H. pylori 26695 gene HP0168"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trainialation="MTQEBLDALMSGGDLENLEALEAKEPAKEPTKEEPKESKENSNY
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DERFPAKKTTTTNRYRIIAENTARAAITPINNDIGKIYTFEKRSYLVLYKILLENNTE
LETTHSGNYNLVRLAPLPAREPERFYTTQVRV"
complement (2268. . 2999)
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/gene="jhp0155"
/note="similar to H. pylori 26695 gene HP0169"
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/db_xref="GI:4154671"
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/product="putative"
/protein_id="AAD05736.1"
/db_xref="G1:4154669"
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complement(3069. .4160)
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales, Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales, Helicobacteracea; Helicobacter.

E. (bases Lto 10085)
Smith, D. R., Noonan, B., Guild, B.C., deJonge, B.L., Carmel, G., Tummino, P.J., Caruso, A., Uria-Nickelsen, M., Mills, D.M., Ives, C., Gibson, R., Merberg, D., Mills, S.D., Jiang, Q., Taylor, D.E., Vovis, G.F. and Trust, T.J.

Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
Nature 397 (6715), 176-180 (1999)
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Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidney Street, Cambridge, MA 02139, USA
Address all correspondence to: hp@arcb.us.astra.com or Richard A. Alm. Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills, Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and Diane E. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta, Canada, T6G 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative identifications, sequence alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web site. (URL: Lecation/Qualifiers).
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Helicobacter pylori, strain J99 section 15 of 132 of the complete
                                                                                                                  60/061958 PI
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GENELABS TECHNOLOGIES INC
PN JP 201517091-A/39
PD 02-0CT-2001
PF 25-APR-1998 JP 1998547263
PR 25-APR-1999 US 60/045107,14-OCT-1997 US 60/0714751707,14-OCT-1997 US C12N15/31,CO7N14/205,CO7N16/12,AG1N39/106
CC Strandedness: Single;
CC Strandedness: Single;
FH Key Loology: Lineart Location/Qualifiers
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95.8%; Pred. No. 8.4;
ive 0; Mismatches
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AE001454.1 GI:4154666
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23; Conservative
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KEYWORDS
SOURCE
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KSEILDYQDGEEAGIKGVAFIIKGENAYGYLKNENGVHRLVRISPFDANAKRHTSFAS
VQISFELDDDIDIEJDEKDVRYDYYRASGAGGOHVNKTESAVRITHFPTGIVVQCQND
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COMPLEMENT (4221. .5393)
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LAQLNOSIIIGLEGNELSCLLYLRVLLLPLERLSLNNOFKLKPFKAQINAPLKLNN
RTHLILGNYSNHQFIPYNNRYESGAIQALAQVDSIALIDEGVGLVQGBIEILRFEN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPEFKAMMEAVKKOALVEFWAKKOAEEVKKIOIPEKEMODFYNANKOOLFVKOEAHAR
HILVKTEDEAKRIISEIDKOPKAKKEAKFIELANRDTIDPNSKNAONGGDLGKFOKNO
MAPDFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKOSPVTYTYEQAKPTIKGMLOEK
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complement(5403..6170)
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                                                                                                                                                                  complement (4221. .5393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="fliR"
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                                                                                                                    'gene="moeA"
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1 (bases 1 to 11193)
Deppenmeier, U., Johan, A., Hartsch, T., Merkl, R., Schmitz, R.A., Martinez-Arias, R., Henne, A., Wiezer, A., Baeumer, S., Jacobi, C., Brueggemann, H., Lienard, T., Christmann, A., Boemecke, M., Steckel, S., Bhattacharyya, A., Lykidis, A., Overbeek, R., Klenk, H.-P., Gunsalus, R.P., Fritz, H.-J. and Gottschalk, G.
The genome of Methanosarcina mazei: evidence for lateral gene transfer between bacteria and archaea
J. Mol. Microbiol. Biotechnol. 4 (4), 453-461 (2002)
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EAGKPFYWINTTWMFRYHYPEEIRGQAGRWQSEYHDAMIEHDRQYGMMLDLLDELG
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Methanosarcina mazei strain Goel, section 208 of 379 of the
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Methanosarcina mazei Gol
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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    11193
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Pred. No. 2.3e+02;
0; Mismatches 3;
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AE013426 AE008384
AE013426.1 GI:20906421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACU1/472 128403 bp DNA linear HTG 09-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
AC017472
                                                                                                          /trānslation="MKSDFADNTLLALTGAIIMENLINFFKKDKFAMHSGIQLLEASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGDMTRKMVVIKNIADAAEISDAIVNLTETDTGTANMTEPAAYNFTGNMVIVRSTDDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTGNMTNVTTDNMTGVADNVTDNMTGNMTGVTGDQTGNVSNVPLKLESIQBIENDREF
NRMPVYINDGSPAQQDFGMKNNBGDVS FRWTTEDDGNAVLGDALYNNITVNDBAB
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DNATDDTSDDMDDMNDYMGRDDTNNMDEDTGTEGMRENDTDDNAGDDRTNNDM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was identified as CDM:10210908 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a "working draft, sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 5.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.8%; Score 18.2; DB 1;
87.0%; Pred. No. 6.8e+02;
ative 0; Mismatches 3;
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HTG; HTGS PHASE2.
Drosophila melanogater (fruit fly)
Drosophila melanogater
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                                                                                                                                                                                                                        'gene="MM1897"
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Best Local Similarity 87.01
Matches 20; Conservative
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                                                                                                                                                                                           9063.
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Best Local Similarity
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVSDRSVKPEOFGSFLSCI PDEWVRNDVGRIFVQTFERSARRWMGLPSGMCVPEBTCG
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EINCOPSRLDLNDELIFRAKDYELKFCISTDSHSVSDLASMRYGLGQARRSWLEKEDI
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                                                                                                                                                                                                                                                                                                                                  'product="putative transcriptional regulator"
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complement(7813. .8274)
                                                                                                                                       complement (1836. .3155)
                                                                                                                                                                                                                  complement (1836. .3155)
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transl_table=
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31369 ATAACGAAATAACGATAAGCAT 31391

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AC010922.10 GI:50872288

DEFINITION ACCESSION VERSION

ORGANISM

REFERENCE AUTHORS

KEYWORDS

RESULT 12 AC010922/c

Rubin, G.M.

TITLE JOURNAL

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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Direct Submission
Submitted (27-SEP-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
Classes 1 to 163466)
Celniker, S., Carlson, J., Wan, K., Pfeiffer, B., Frise, E., George, R., Hoskins, R., Stapleton, M., Pacleb, J., Park, S., Svirskas, R.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE003504 298641 bp DNA linear INV 15-MAR-2004 Drosophila melanogaster chromosome X, section 56 of 74 of the
INV 31-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley, CA 94720, US Sequence version replaced gi:13324755.

Berkeley, CA 94720, US On Jul 31, 2004 this sequence version replaced gi:13324755.

Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

Berkeley, CA 94720

This sequence submission incorporates changes made during reevaluation of the assembly or fingerprint verification of the clone. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.org/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-JUL-2004) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
                                                                                                                                                                                                                     Eukaryopta, Michael Arthropoda, Hexapoda, Insecta, Pterygota, Bukaryota, Michael Arthropoda, Hexapoda, Insecta, Brerygota, Bepydroidea, Drosophilidae; Drosophilae, Brachycera; Muscomorpha, Ephydroidea; Drosophilidae; Drosophila.

(Dases 1 to 163466)

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butchhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., George, K.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Noshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Peiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="15E-15E"
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Drosophila melanogaster BAC library, partial ECORI in
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   AC010921 163466 bp DNA linear INV 31.
Drosophila melanogaster clone BACR15L12, complete sequence
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/organism="Drosophila melanogaster"
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/strafi=""y; cn bw sp"
/db_xref="taxon;7227"
/chTomosome="X"
                                                                                                                                                               Drosophila melanogaster (fruit fly)
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AE003504 AE002593 AE014298
AE003504.3 GI:22832424
                                                                                              AC010921.12 GI:50872266
                                                                                                                                                                                                    Drosophila melanogaster
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87.0%;
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                              DEFINITION
ACCESSION
VERSION
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SOURCE
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VERSION
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AE003504
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                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster

Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoplera; Endoplerygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 15260),
S (chiker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciestolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S. R., Karra, K., Karra, K.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Madda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (28-SEP-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 4-121, Berkeley, CA 94720, USA
2 (bases 1 to 152607)
Celniker,S., Carlson,J., Wan,K., Pfeiffer,B., Frise,E., George,R.,
Hoskins,R., Stapleton,M., Pacleb,J., Park,S., Svirskas,R.,
Direct Submission
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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This sequence submission incorporates changes made during reevaluation of the sequence submission incorporates changes made during treevaluation of the afformation about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fuifly.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="BAC clone BACR09H01 (D896)"
/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
PBACe3.6)"
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Drosophila melanogaster clone BACR09H01, complete sequence.
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/mol_type="genomic DNA"
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/db xref="taxon;7227"
/chromosome="X"
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Query Match 75.8 Best Local Similarity 87.0 Matches 20; Conservative

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us-10-039-183a-18.rge

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Direct Submission
Submitted (OG-SBE-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
7 (bases 1 to 298641)
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LPPQKSVVIAYLCWLFGGIFGLHHLYLHRDRHAFIWWCTLGGYWGIGWMGELFLIPEY
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LSFLHWTIPLFVSLGVWLVGNIGREQGVWWHCLVAAYLAYPARYLIYDETYSLLLTGL
VAALTFDGLSKQWRRTPPRKGSPGERTFKLITAVIIYCAFWGSPLYFNGTISDEDGGE
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GVSATASQAEITAAYRKLSKEYHPDKVKDEGLRAQAHQRFIEIQQAYSVLSKIKSNRR
                                                                                                                                                                                                                                                                           5 (bases 1 to 298641)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
6 (bases 1 to 298641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-MR-2004) FlyBase, Harvard University, Biological Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA On Sep 13, 2002 this sequence version replaced gi:10728299.
                               Kaminker, J.S., Bergman, C.M., Kronmiller, B., Carlson, J., Svirskas, R., Patel, S., Frise, B., Wheeler, D.A., Lewis, S.E., Rubin, G.M., Ashburner, M. and Celniker, S.E.
The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective Genome Biol. 3 (12), RESEARCH0084 (2002)
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complement(join(651. .2145,2658. .2980))
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complement(907. .2127)
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db_xref="FLYBASE:FBgn0030806"
:omplement(3729. .4736)
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/locus taq="CG13001"
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product="CG9089-RA"
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Ralpern, A., Patel, S., Adams, M., Champe, M., Dugan, S. P., Frise, E.
Hodgson, A., George, R. A., Hoskins, R. A., Laverty, T., Muzny, D. M.,
Nelson, C. R., Pacleb, J. M., Park, S., Pfeiffer, B. D., Richards, S.,
Sodesgren, B. J., Svirskas, R., Tabor, P. E., Wan, K., Stapleton, M.,
Sutton, G. G., Venter, C., Weinstock, G., Scherer, S. E., Myers, E. W.,
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   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Ebkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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SOURCE
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see http://www.nanger.ac.uk/Projects/L major/
CDS are numbered using the following system eg L7171.01. L7171
(cosmid name), 01 (first CDS)
To make the cosmid library Leishmania major Friedlin DNA was
partially digested with Sau3AI prior to cloning into BamHI site of
the cosmid shuttle vector cLHTG (Ryan et al. 1993 Gene
131:145-150). The sequence of the packaged vector was determined by
Peter Myler and Ken Stuart at Seattle Biomedical Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation codon. Transmembrane domains were predicted as implemented at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integral part of the ACEDB-based analysis tools for the C.elegans integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of leishmania sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                        Submitted (07-DEC-1999) European Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 18A, (E-mail: barrell@sanger.ac.uk) and Universitat degli Studi di Trieste-Lab. di Genetica, P.zzale Valmaura, 9, 34148 Trieste ITALY see http://www.ebi.ac.uk/parasites/leish.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for
CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute, and is available as accession number U59231. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the FramePlot program of Bibb et al.,

Gene 30:157-166(1984) as implemented
at http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl. (2)

codon preference based on the codon usage table for Leishmania at

http://www.kazusa.or.jp/codon/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/
IMPORTANT: This sequence MAY NOT be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions. Cosmid L7771 is
overlapped by L3640.
1 (bases 1 to 37578)
Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
Smith,D.F.
                                                                                                                                                                                                                                                           Ivens, A.C., Murphy, L., Quail, M.,
                                                                                                          A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major"
                                                                                                                                                                                                                             2 (bases 1 to 37578)
Tosato, V., Bruschi, C.V., Ivens, A.
Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="Friedlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="tottottoottttt"
/label=tottottoottttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene prediction is done using:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (185. .199)
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                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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gene="RhogAP15B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="CG4937"
/product="CG4937-RA"
/db_xref="FLYBASE:BBGN0030808"
join[13401. 15422,15482. 15608,15668. 16308,16540. 16635,
16690. 16824,16901. 17424,17483. 17618)
                                                     /db_xref="Flynbade:FBgn0030807"
/translation="MSISLSEFYQSSLIFWSHLIHILLQFIQTNCWNHITQKEQQQEE
LNBFCAISKTWDAFVEEQQKRYQRKSHEYAKVELLHRLLVQQQLQELEQRRLIRLALA
RRRLDYSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDLDRRQTMPSTEVFNTIQFSSPLNRNGGLPDLRENDAKLQKED
YLRPDPDQEDDGCYEVPKTQGKPPSYDEALRSRPSPSDSPMSRNLAQEAAQLVQLRNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major Friedlin chromosome 21 cosmid L7171.
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db_xref="G1:22832425"
db_xref="FLYBASE:FBgn0030808"
                                                                                                                                                                                                                                                                                                                                        /db_xref="FLYBASE:PBGN0030807"
/db_xref="FLYBASE:PBGN0030807"
complement(<10262. .>10594)
/locus_tag="CG13000"
/product="CG13000-RA"
/db_xref="FLYBASE:FBGN0030807"
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                                                                                                                                                                                                                                                  /locus tag="CG13000"
/map=15C4_15C4"
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75.8%; Score 18.2; Di
Best Local Similarity 87.0%; Pred. No. 5e+0:
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10262. .10594)
/locus_tag="CG13000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAF48685.1"
db_xref="GI:7293305"
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/map="15C4-15C4"
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gene="RhoGAP15B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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LMFL7171/c
LOCUS
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complete sequence; 74% identity over 76 bases; bases 1480. .1543 AL031910 Leishmania major Friedlin chromosome 4 cosmid L2743; 81% identity over 63 bases; bases 1480. .1543 AL031910 Leishmania major Friedlin cosmid L2743; 81% identity over 63 bases; bases 36538. .36712 AF008205 Leishmania major chromosome 1, complete sequence; 74% identity over 74 bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="region of BLASTN similarity to bases 70684. .70753 APO80205 Leishmania major chromosome 1, complete sequence; 78% identity over 69 bases; bases 32685. .32761 AC005836 Leishmania major chromosome 3 clone L509 strain Priedlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
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                                                      /gene="1717.0"
/note="predicted TM helix region"
complement(2866. .2922)
/gene="1717.01"
/note="predicted TM helix region"
complement(2983. .3039)
/gene="1711.01"
                                                                                                                                                                                                                                                                                             'note="predicted TM helix region"
/note="predicted TM helix region"
complement(2788. .2856)
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/note="cctcctctctctctctcc"
/label=cctcctctctctctctcc
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/note="tcttccttcttc"
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/note="tottttctttttttc"
/label=totttttttttc
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/note="ctctccctccttcc"
/label=ctctcccctccttcc
                                                                                                                                                                                                                                                                                                                                   complement (3313. .3329)
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                                                                                                                                                                                                                                                 Complement (1276. 3165)

/ Gene="L7171.01"

complement (1276. 3165)

/ Gene="L7171.01"

complement (1276. 3165)

/ Gene="L7171.01"

/ Note="L7171.01"

/ Note = Note | 
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/translation="MPSCGTSLVSGLKKLGKPIFSQTREVQORKEKGLHPVSELRRFH
/translation="MPSCGTSLVSGLKKLGKPIFSQTREVQORKEKGLHPVSELRRFH
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FVIVLPPYIVNWWRRQGKTPEQIAALKATVIYYERKFVPMPRLIVGFYAVLLLLVFFT
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BAARTKUDDBCGRLVQLDDLCQEVRTSNEGSGSVLEPRINATVGTGTSSQSEDVINRY
AHQDPRYEGTVKDYLLNIDVWLIMLLFVCYGCMGVIVLYNSSTISIALTGHKRSIQLS
ALYTARLGVGSSVGRTAFGLFRAYVQHQEPERIRKVLVSBALFVSBAMAFLAGIFELFLF
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GRTIDREQRRLHIPMDRECNVKSCVRTPIIVSTVLAFFGVLVALAIHPRYAAFVKRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="hypothetical protein L7171.01"
protein id="CAB62804.1"
db_xref="GI:6562648"
                                                      note="predicted TM helix region"
complement (1561. .1629)
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complement(1642, .1710)
/gene="L7171.01"
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//gene="L1171.01"
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/gene="L7171.01"
/note="predicted TM helix region"
complement (1468. .1536)
/gene="L7171.01"
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complement(2218. .2286)
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complement(2695..2751)
/gene="L7171.01"
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complement(2317. .2385)
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complement (2497. .2565)
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complement (2584. .2652)
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76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
                AC136189 Homo sapi
Continuation (6 of
AC134998 Homo sapi
AC132329 Mus muscy
AC46177 Homo sapi
AC122826 Mus muscy
AC122826 Mus muscy
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AO1MA3/04, AO1MS9/16, AG1K9/48, AG1K31/70, AG1K31/715, AG1K39/02,
AG1K39/40,
GO1N33/554, GO1N33/569
Strandednegs: Single,
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AC139810 Homo sapi
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
I (bases 1 to 31)
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
Febra, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polymucleotide molecules
Patent: JP 2001523954-A 60 27-NOV-2001;
PN ACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC
PN 27-NOV-2001
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HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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BX897661
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BX005126
BX547938
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    .31
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/db_xref="taxon:10509"

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AC107303
BX897661
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BX005126
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Matches 31; Conserv
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AC017240 Drosophil
AC009741 Drosophil
AE003695 Drosophil
Continuation (7 of
AL935255 Lactobaci
AL9354814 Zebrafish
CR376780 Danio rer
CR293523 Danio rer
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BD009865 Proteins,
AE000626 Helicobac
AE001541 Helicobac
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                                                               April 23, 2005, 17:27:10 ; Search time 804.69 Seconds (without alignments) 1866.696 Million cell updates/sec
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AL935255
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Copyright (c) 1993
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Helicobacteracaes, Helicobacter.

Knapp, B., Hundt, E. and Schmidt, K.H.
Proteins, in particular membrane proteins, of Helicobacter pylori, their preparation and use broteins and use their preparation and use to their pylori pylorisms.

CHIRON BERNIAG GMBH & CO OS Helicobacter pylori, ph. 06-MAR-2001

PP 25-JUL-1997 JP 1998508651

PR 26-JUL-1996 DE 196 30 390.7

PI BERNHARD KNAPP, ERIKA HUNDT, KARL HEINZ SCHMIDT PC CIL2N15/31, CO7K14/205, CO7K16/12, GO1N33/53, AG1K31/70, AG1K39/106, PC AG1K39/395

CC Strandedness: Single;

CC Topology: Linear;

FH Key L. 2825

FT Source L. 2825

FT Source L. 2825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BD009865 2825 bp DNA linear PAT 31-JAN-2002 Proteins, in particular membrane proteins, of Helicobacter pylori,
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JP 2001502886-A/6.
Helicobacter pylori
Helicobacter pylori
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
                   PI
                                                       AWAL AL GARAWI
A01N13/04,A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,A61K39/40,A01N33/54,G01N33/569
Strandedness: Single,
Topology: Linear;
                   HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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Location/Qualifiers
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Matches 31; Conservative 0; Mismatches 0; Indels
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    .2825
    ^organism="Helicobacter pylori"
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|db_xref="taxon:210"

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                                                                                                                                                                                                                      1. .1448
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31-MAR-1998 JP 1998541962
                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Best Local Similarity
                       MILLER,
MILLER,
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BD009865/c
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                                                                                                                                         BD082355 31 bp DNA linear PAT 27-AUG-2002 76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
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A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
A01K39/30,A01N33/569
G01N33/554,G01N33/569
Strandedness: Single;
Froplogy: Linear;
Key
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae.

Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polynucleotide molecules
Patent: JP 2001523954-A 54 27-NOV-2001;
MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
HUMAN GENOME SCIENCES INC
PU JP 2001523954-A/54

PD 27-NOV-2001
                                                                                                                                                                                                                                                                                     Mastadenovirus Viruses, no RNA stage; Adenoviridae.

Viruses; deDNA viruses, no RNA stage; Adenoviridae.

Klases 1 to 31)

Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.

K kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polymuclectide molecules

Patent: JP 2001523954-A 62 27-NOV-2001;

PRERIBUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET WACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA, HUMAN GENOME SCIENCES, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP 2001523954-A/62
21-NOV-2001
31-MRR-1998 JP 1998541962
HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polynucleotide molecules.
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    GCTAATATTATTCAATAATATTGCTCACAAC 31
                                        GCTAATATTATTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTAATATTATTCAATAATATTGCTCACAAC 31
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JP 2001523954-A/54.
                                                                                                                                                                                                                          GI:22627965
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BD082355.1 GI:2262
JP 2001523954-A/62.
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PD 27-
PD 11-
PD HARA
MILLER,
PI AMA
PC A01
PC A01
PC A01
CC SCT TOP
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BD082347/c
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TITLE
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KEYWORDS
SOURCE
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/brotein id="AADO8247.1"
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EST KNGRIDDDVITATPDMMAVVGKVGRILGPKGLMPNPKTGTVTMDIAKAVSNAKSG
QVNFRVDKKGNYHARQKASFPEEKIKENMLELVKTINRLKFSSAKGKYIRNAALSLT
MSPSYSLDAQELMDIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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GB:U00096 PID:1790414 percent identity: 41.04; identified
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trocte="similar to SP:P23375 percent identity: 55.10; identified by sequence similarity; putative"
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complement (3242. .3314)

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complement (3242. .3314)

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                                                                                                                                                                                                                           /gene="HP1201"
complement(1168. .1872)
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                                                                                                                                                                                                             Helicobacter pylori 26695

Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales, Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter.

E 1 (bases 1 to 10532)

S Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A., Sutton,G.G., Fleischmann,R.D., Ketchum,K.A., Klenk,H.P., Gill,S., Kirkness,E.F., Dougherty,B.A., Nolson,K., Quackenbush,J., Zhou,L., Kirkness,E.F., Glodek,A., McKenney,K., Fitzegerald,L.M., Lee,N., Adms,M.D., Hickey,E.K., Berg,D.E., Googyme,J.D., Utterback,T.R., Peterson,J.D., Kelley,J.M., Karp,P.D., Smith,H.O., Fraser,C.M. and Venter,J.C.
                                                         AB000626 10532 bp DNA linear BCT 06-APR-1999
Helicobacter pylori 26695 section 104 of 134 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Fleischmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Bougherty, B.A., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, E.F., Peterson, S., Loftus, B., Richatdson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.E., Gocayne, J.D., Uterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, O. Direct Submission
Direct Submission
Submitted (17-MAR-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 10532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(142. 519)
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protein id="AAD08245.1"

db xref="G1:2314361"
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AE000626.1 GI:2314360
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                                                                                                                                      ACCESSION
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  RESULT 5
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Libert Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidney Street, Cambridge, MA 02139, USA Address all correspondence to: hp@arcb.us.astra.com or Richard A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills, Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Gin Jiang and Diane E. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta, Canada, TGG are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative identifications, sequence alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web site. (URL: http://www.astra-boston.com/hpylori).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEFPGDDTPIVAĞSALRALEEAKAĞNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLM
VEDDVEJRASIYYYYGVERREKEKSEK
GDNVGVLLRGTKKEEVRRGMYLCKPGSITPHKKPEBEIYVLSKEEGGHHTPFFNYRR
OFYVRTIDTGSITLEPGGEMMPGDNVKITVELISPVALELGTKPAIREGGRTVGAG
                               Helicobacter pylori J99
Helicobacter pylori J99
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteracae; Helicobacter.
1 (bases 1 to 15292)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cranslation="makekfnrtnphvnigtighvyhgkttlsaaisavlslkglaem
KDYDNIDNAPQEKERGITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGA
ILVVSAADGPMPQTREHILLSRQVGVPHIVVFLNKQDMVDDQELLELVEMEVRELLSA
                                                                                                                                                                                                                                                                                                                                                                                                      Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pyloxi
Nature 397 (6715), 176-180 (1999)
                                                                                                                                                                                                                     Alm, R.A., Ling, L.S., Moir, D.T., King, B.L., Brown, B.D., Doig, P.C., Smith, D.R., Noonan, B., Gulld, B.C., deJonge, B.L., Carmel, G., Tumino, P.J., Caruso, A., Uria-Nickelsen, M., Mills, D.M., Ives, C., Gibson, R., Merberg, D., Mills, S.D., Jiang, Q., Taylor, D.E., Vovis, G.F. and Trust, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to H. pylori 26695 gene HP1204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to H. pylori 26695 gene HP1205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon start=1
/transI table=11
producE="ELONGATION FACTOR TU (EF-TU)"
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protein id="AAD06710.1"
db xref="G1:4155730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Helicobacter pylori J99"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            King, B.L., Alm, R.A. and Trust, T.J. Direct Submission
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complement (257. .415)
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complement (462. .1661)
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'db_xref="G1:4155731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:85963"
complement(257. .415)
/gene="rpmG"
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/transl_table=11
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                                   SOURCE
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GDNVQVLLRGTKKEEVERGMYLCKPGSITPHKKFEGEIYVLSKEEGGHHTPFFINYRP
QFYVRTTDVTGSITLPEGVENVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAG
VVSNIIE"
                                                                                                                                                                                                                                                                                                                                                                       /protein id="AAD08250.1"
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/db_xref="G1:23146
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Helicobacter pylori, strain J99 section 102 of 132 of the complete
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                                                                                                                                                                                     /note="similar to SP:P42482 PID:587590 percent identity:
89.50; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                /codon start=1
/transl_table=11
/product="translation elongation factor EF-Tu (tufB)"
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protein id="AAD08251.1"
db_xref="GI:2314367"
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Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="codon recognized: ACC"
complement(4982. .5055)
//gene="tRNA-GJy-2"
complement(4982. .5055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="codon recognized: GGA"
complement(5074. .5155)
/gene="tRNA-Tyr-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="codon recognized: UAC"
complement (5186. .5258)
/gene="tRNA-Thr-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3541 GCTAATATTATTCAATAATATTGCTCACAAC 3571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTAATATTATTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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/gene="tRNA-Thr-1"
complement (4877. .4948)
/gene="tRNA-Thr-1"
/product="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tRNA-Gly-2"
/product="-
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/gene="tRNA-Thr-2"
                                       complement (3548. .4747)
                                                                                                                  complement (3548. .4747)
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/gene="tRNA-Tyr-1"
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/gene="HP1206"
5448. .7184
/gene="HP1206"
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Matches 31; Conservative
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gene

trna

gene **ERNA** gene

CDS

gene **trna**

gene **trna** WSNIIE"

genome. AE001541 AE001439 AE001541.1 GI:4155724

DEFINITION ACCESSION VERSION

AE001541 LOCUS

RESULT 6

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Query Match

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/product="O-SERINE ACETYLTRANSPERASE"
/protein id="AAD06715.1"
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VTLGGTGKFKGKRHPTLGNEIHPGAKVGALCVGDDVRIGANAVVLSDLFTGSTAV
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LYBEAFTPYQNELLFKEGEGIVLNERLLDLLKNQYFDEIIKGIESSALSERENVFKEV
AKKISEAHSEFSLEEIELSLEKVKKTEIRRMIIQDKIRPDKRALEEVRPISIESNLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tränslation="mKFLALFFLALAGVAFAHDGGMGGMDM1KSYSILGAMIGLGIAA
FGGAIGMGNAAAATITGTARNPGVGGKLLTTMFVAMAMIEAQVIYTLVPAIIAIYSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="mdfitinsgnrteefalkqvakqatsslmyrlgktlilasvcve
REPVSEDFLPLVVQFLEKSYAAGKIPGGFVKREGRAQDFEILTSRLIDRTLRPLFPKD
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1. (Dasses I to 968)
Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.
Antigenic composition and method of detection for Helicobacter
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|transl_table=11
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7507 . 7602
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/noce="similar to H. pylori 26695 gene HP1211"
/codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to H. pylori 26695 gene HP1212"
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(transl_table=11
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complement(7804. .8121)
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complement (8254. .10320)
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RYSIETVGFSLLILAVAYILFKYGGARMVLPTISMYALLALYRILPSVTGVISYYNEIA
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AFKRAKKASQKELILKGAHPPVSLANNEVYQDSNDLIGKASGDILLLDPPVNARQY
GANYHLINTIAAYTPPTPKGKTDLESYQNSFCSRFQILNAFENLIKKARFKYIFLSY
NNEGLMSETEIKNILKKYGAYSLVYTYMRFKADNKRAHKAVHTKECLHVLIK"
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TALLICHSGOGKSTLADIINGLYPYSSOEIPIUNTLLYSENRSWRKKGSTROYIOPINYL
PDGTVGDNIAPGSAIDERKLIKVCKMAHIYDPLCEHEGLKTOVGEGGAKLSGORKQRI
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                                                                                                                                                    H. pylori 26695 gene HP1206"
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/trans1_table=11
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(WETHYLTRANSFERASE)"
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/note="aynonym: jhp1131"
complement(4966. .5955)
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/gene="jhp1130"
complement (4110. .4778)
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                                                                                                                                                    'note="similar to
/gene="jhp1129"
/gene="jhp1129"
/gene="jhp1129"
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'codon start=1
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/transl_table=11
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gene="jhp1129"
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Birren, B., Nuebaum, C. and Lander, E.
Mus musculus chromosome 14, clone RP24-14314
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Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
                                                                                                                                                                                            Legrain, P., Rain, J.C., Colland, P., de Reuse, H. and Labigne, A. Protein-protein interactions in Helicobacter pylori Patent: WO 02066501-A 5598 29-AUG-2002; Hybrigenics (FR); INSTITUT PASTEUR (FR)
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AC102439.3 GI:45680590
HTG; HTGS_PHAREI; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
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Pred. No. 2.8e+02;
0; Mismatches 1;

    .30
        /organism="Helicobacter pylori"
/mol type="unassigned DNA"
/db_xref="taxon:210"

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             AX793134.1 GI:32958581
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Best Local Similarity 96.3%;
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Antigenic composition and method of detection for Helicobacter
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other sequences,
1 (bases 1 to 970)
Chow,T.P., Fry,K.E., Lim,M.Y. and Mcatee,C.P.
Antiganic composition and method of detection for Helicobacter
Patent: JP 2010151791-A 332 02-0CT-2001;
GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Datent: JP 2001517091-A 201 02-OCT-2001;
GENELABS TECHNOLOGIES INC
PN JP 2001517091-A/201
PD 02-OCT-2001
PP 25-APR-1997 US 60/045107,14-OCT-1997 US
THERESA P CHOW, KIRK B FRY, MOON Y LIM, C P MCATEE PC
C12N15/31,C07K4/205,C07K16/12,A61K39/106
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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PP 25-APR-1997 US 60/045107,14-0CT-1997 US

THERESA P CHOW, KIRK E FRY,MOON Y LIM, C P MCATEE PC

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FY Key Location/Qualifiers.
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/mol type="genomic DNA"
/db xref="taxon:32630"
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/organism="synthetic construct"
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Direct Submission

Burnetted (14-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Essearch, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Cool, Ymore, A., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grander, P., FitzGerald, M., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Ilier, Y., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Indolad-Toh, K., Liu, X., Lui, A., Mabbltt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Weldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Plerre, N., Ramasamy, U., Raymond, C., O'Connor, T., O'Donnell, P., O'Neil, D., Ollver, J., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, M., Stolanovic, N., Stubbs, M., Valamss, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wasilliev, H., Voung, G., Zainoun, J., Zembek, L., Zahme, A. and Zody, M.
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Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 21295)

8 Birran, B. Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M. Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cook, P., Cornim, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Malenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Ocomor, T., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                        Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 3, clone RP23-335P23
                      Mus musculus (house mouse)
                                                                                                                                                                                              (bases 1 to 212995)
             SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Perreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Micol, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Micol, P., Micol, F., Norbu, C., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zanbek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence submission@genome.wi.mit.edu ------ Project Information Center project name: L18796
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/clone_lib="RPCI-24 Male Mouse BAC"
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/db_xref="taxon:10090"
/chromosome="14"
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AUTHORS
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AC017240
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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J. Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Submitted (18-03M-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 28, 2004 this sequence version replaced gi:38524693.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                         ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: 120348
Center clone name: 335_P_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP23-335P23"
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6108 .6230
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6231. .6325
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34. .39
                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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complement (4912. .4901)
rpt family="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement (430...587)
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/rpt_family="(CA)n"
998. .2042
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ACO17240 120794 bp DNA linear HTG 09-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
AC017240
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster (fruit fly)
Brosophila melanogaster (broit fly)
Brosophila melanogaster (broit fly)
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Enydyroidea; Drosophilidae; Drosophila.
I (bases 1 to 120794)
Adams,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.8%; Score 23.2; DB 10; Length 212995; 89.3%; Pred. No. 1.5e+02;
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                                                                                                                                    22532 TAATATTATTCAATAATATTGTTTAAAA 22505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17964. .18160
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19418. .19438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TAATATTATTCAATAATATTGCTCACAA 30
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complement(8996. .9212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20450. .20737
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6132. .16240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celulker, S. B., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Chempe, M., Clavez, C., Chew, M., Ciestolka, L., Doyle, C.M., Farfan, D.B., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, B., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Marda, P., Lee, B., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pefeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Suirs, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Direct Submission
Submitted (19-DBC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10209984 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120794;
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Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22.8; DB 2;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.5%; Score 22.8; D
Best Local Similarity 92.3%; Pred. No. 2.4e
Matches 24; Conservative 0; Mismatches
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AC009741.5 GI:13096041
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VERSION
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AC009741/c
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Bradoterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophila;

CE (Dases 1 to 225655)

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,

Amanatidea; P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Henderson,S.N.,

Button,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,

Burton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,

Burton,G.G., Mortman,J.R., Yandell,M.D., Nelson,C.R., Gabor,G.L.,

Abril,J.F., Agbayani,A., Dasendale,J., Belanckoh,C.R., Gabor,G.L.,

Burtis,K.C., Busan,D.A., Berman,B.P., Bhandari,D., Bolshakov,S.,

Burton,G.G., Mortman,R., Buuler,H., Cadieu,E., Center,A.,

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Burtis,K.C., Busan,D.B., Deller,A., Downes,M., Dugan-Rocha,S.,

Duckov,B.C., Dunn,P., Dutbin,K.J., Expensed,C., Ferrac,C.,

Ferriera,S., Fleischmann,W., Fosler,C., Gabrielian,A.E.,

Gelbart,W.M., Glasser,K., Glodek,A., Gong,P., Gorrell,J.H., Gu,Z.,

Kravitz,S., Kulp,D., Lai,Y., Houston,K.A., Howland,T.J.,

Moin,P., Harris,M., Harris,N., Houston,K.A., Kolbri,D., Hall,Y., Macha,C.,

Li,J., Li,Z., Liang,Y., Lin,X., Math,P., Morton,B., Mortholy,D.,

Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,

Musskern,D.R., Pacleb,J.M., Palazzolo,M., Pittuan,G.S., Pan,S.,

Pollard,J., Puri,V., Reese,M.G., Reinert,K., Tector,C., Turner,R.,

Stapleton,M., Skupski,M.P., Salns,H., Toctor,C., Turner,R.,

Stapleton,M., Skupski,M.P., Salns,H., Toctor,C., Turner,R.,
shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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Drosophila melanogaster chromosome 3R, section 33 of 118 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 166863;
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Pred. No. 2.2e+02;
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AE003695 AE002708 AE014297
AE003695.2 GI:23171087
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il Similarity 92.3%;
24; Conservative (
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Best Local Similarity
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us-10-039-183a-15.rge

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EIPQNHNGKVYRRYRAEDLFYALSKKN"
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HEADPNVLCLSSSGSTSLWFPLLP1VMPQAAGRVTSAERKSP1QEPVEKTATTTPTRK
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Rubin, G.M. and Lewis, S.E.
Annotation of the Drosophila melanogaster euchromatic genome: a systematic review
Genome Biol. 3 (12), RESEARCH0083 (2002)
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Submitted (O6-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
7 (bases 1 to 225655)
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 225655)

Celniker,S.B., Wheeler,D.A., Kronmiller,B., Carlson,J.W.,
Halpern,A., Patel,S., Admas,M., Champe,M., Dugan,S.P., Fise,E.,
Hodgson,A., George, A.A., Hoskins,R.A., Laverty,T., Muzny,D.M.,
Nelson,C.R., Pacleb,J.M., Park,S., Pfeiffer,B.D., Richards,S.,
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Sutton,G.G., Venter,C., Weinstock,G., Scherer,S.E., Myers,E.W.,
Gibbs,R.A. and Rubin,G.M.
Finishing a Whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence
Genome Biol. 3 (12), RESEARCH0079 (2002)
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Submitted (10-MAR-2004) FlyBase, Harvard University, Biological
Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA
On Sep 18, 2002 this sequence version replaced gi:7299572.
Location/Qualifiers
Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weissenbach, J., Williams, S.M., Woodager, Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F. Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, K.Y., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA 6 (bases 1 to 225655)
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The transposable elements of the Drosophila melanogaster
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Genome Biol. 3 (12), RESEARCH0084 (2002)
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YEGTSEIQRIVIANAVLRELGKE"
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WPCOMMENT
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Query Match 72.9%; Score 22.6; DB 1; Length 110000; Best Local Similarity 86.2%; Pred. No. 2.9e+02; Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Search completed: April 24, 2005, 03:21:50 Job time : 812.69 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                    4390206 seqs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav07972 Helicobac	Aav07970 Helicobac	Aav07964 Helicobac	Aav90742 Nucleotid	Aav90873 Nucleotid	Abx69371 Novel Hel	Aas53681 Helicobac	Aca34860 Prokaryot	Aav07968 Helicobac	Abn79830 Fungal ZB	Abn79831 Fungal ZB	Abz10049 Haematopo	Abz10195 Haematopo	Aas45406 Chemicall	Abl33502 Human imm	Abk28255 DNA trans	Adf77343 Lactic ac	Adq08665 Ciona int	Aaa79704 Eucalyptu	Aah76178 A. thalia
SUMMARIES	ΙD	AAV07972	AAV07970	AAV07964	AAV90742	AAV90873	ABX69371	AAS53681	ACA34860	AAV07968	ABN79830	ABN79831	ABZ10049	ABZ10195	AAS45406	ABL33502	ABK28255	ADF77343 00	ADQ08665	AAA79704	AAH76178
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	Score	31	31	31	29.4	29.4	25.4	24	24	21.6	21	21	21	21	21	21	21	20.6	20.2	20.5	20
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Adr6176 A. thalia Adr68103 Full leng Abl12454 Drosophil Abl3002 Human imm Aah20175 Mouse spa Acn4118 Human gen Continuation (1 of Continuation (1 of Abn70726 Etreptoco Abn70726 Etreptoco Abn70756 Freptoco Ad55609 Human CDN Aq06168 Encodes H Aqq32854 BMP5. 3/2 Aqq32854 Human BmP Axc95262 DNA encod Abk64540 Human ben Acc56729 Human bon Acc56729 Human bon Ad56525 Human bon Ad56525 Human bon Ad56525 Human con Ad56525 Human con Ad56525 Human con
AAH76176 AAH76176 ABL12454 ABL133002 AAH20175 AAH20175 AAH20175 AAN70726 AAN70727
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ALIGNMENTS

AAV07972 standard; DNA; 31 BP

RESULT 1

AAV07972;

GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR; Algarawi A; Helicobacter pylori polypeptide GHPO 750 3' DNA primer. Tomb J, Miller C, (INWR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC. 97US-00831310. 97US-00834666. 98WO-US006421. (revised)
(first entry) Kleanthous H, Lissolo L, WPI; 1998-568251/48. Synthetic. Helicobacter pylori. 31-MAR-1998; 01-APR-1997; 01-APR-1997; WO9843479-A1 08-OCT-1998. 25-MAR-2003 02-FEB-1999 primer; ss.

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases. Claim 5; Page 156; 184pp; English.

This 3' primer is used with a 5' primer (see AAV07971) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07964) encoding the a 50 kDa polypeptide (see AAW73035) designated GHPO 750. The isolated polynucleotide, and encoded

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GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; ss.
                                                                                                        Helicobacter pylori 50 kDa polypeptide GHPO 750 DNA.
                                                                                                                                                                                                                                                                                                                  (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC.
                    AAV07964/c
ID AAV07964 standard; DNA; 1448
                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                    Kleanthous H, Lissolo L,
                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-568251/48.
                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW73035.
                                                                                                                                                                                                                                                              31-MAR-1998;
                                                                                                                                                                                                                   WO9843479-A1
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                                                                        25-MAR-2003
02-FEB-1999
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                                                    AAV07964;
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                                                                                                                                                                         Key
          RESULT 3
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polypeptide, can be used to develop vaccines for the treatment and
prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct
PI field.)
                                                                                                                                                                                                                                                                                               GHPO 1360; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This 5' primer is used with a 3' primer (see AAV07970) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07963) enceding the mature form of a 32 kDa polypeptide (see AAW73034) designated GHPO 1360. The isolated polymoleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter infections. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
                                                                                               Gaps
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                                                                        DB 2; Length 31; 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomb J, Miller C, Algarawi A;
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                                                                                              0; Indels
                                                                                                                                                                                                                                                                         Helicobacter pylori polypeptide GHPO 1360 5' DNA primer.
                                                    Sequence 31 BP; 12 A; 6 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31 BP; 12 A; 6 C; 2 G; 11 T; 0 U; 0 Other;
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(HUMA-) HUMAN GENOME SCI INC.
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100.0%; Pred. No. v.-
0; Mismatches
                                                                                                                    1 GCTAATATTATTCAATAATATTGCTCACAAC 31
                                                                                                                                 GCTAATATTCAATAATATTGCTCACAAC 31
                                                                        100.0%; Score 31; DB
100.0%; Pred. No. 0.1
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003 to correct PI field.)
                                                                                                                                                                                               AAV07970 standard; DNA; 31 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00831310
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                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kleanthous H, Lissolo L,
                                                                                              31; Conservative
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                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                 Similarity
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1998;
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02-FEB-1999
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                                                                                                                                                                                                                                                                                                          primer; 88.
                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                    AAV07970;
                                                                         Query Match
Best Local &
                                                                                               Matches
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AAV07970
          888333
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Algarawi A;

Tomb J, Miller C,

Location/Qualifiers 118. .1317 /*tag= a

98WO-US006421 97US-00831310 97US-00834666

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                                                                                                                                                                                                                                  This DNA sequence codes for a 50 kDa Helicobacter pylori polypeptide (see AAW73015) designated GHPO 750. A polynucleotide encoding GHPO 750 can be obtained from genomic DNA by PCR amplification (see AAW7971-72. The invention provides polynucleotides (see AAW72001, AAW07912-21 and AAW73022-32), GHPO 750 and a 32 kDa polypeptide (see AAW73034). These polynucleotides were initially identified in a search of H. pylori genomic databases. DNA cassettes for expression of the Helicobacter proteins (unprocessed or mature forms) in prokaryotic or eukaryotic cells are provided. The polynucleotides can be used in vaccines to prevent or are provided.
New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treat Hb infection in a mammal. Viral (especially poxvirus) or bacterial vectors are used. Products and methods of the invention allow treatment and prevention of gastroducdenal diseases associated with Hb infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and atrophic gastritis, and peptic ulcer methods are also provided. GHPO 750 was demonstrated to be a protective antigen. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1448 BP; 466 A; 237 C; 364 G; 381 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1324 GCTAATATTATTCAATAATATTGCTCACAAC 1294
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                                                                                                                                                                         Claim 1; Page 150-152; 184pp; English.
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1es 31; Conservative
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AAV90742/c

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Gaps

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GCTAATATTATTCAATAATATTGCTCACAAC 31

1 GCTAATATTCAATAATATTGCTCACAAC 31

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31; Conservative

AAV90742;

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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H: pylori-positive antisers. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diaeases (gastritis, peptic ulcer, gasinst H. pylori infection and related diaeases (gastritis, peptic ulcer, gasinst Codenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                   New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein-protein interaction; ulcer; selected interacting domain; SID;
PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 970 BP; 306 A; 155 C; 261 G; 248 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Reuse H, Labigne A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.4; DB 2;
Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Helicobacter pylori gene PCR primer #2342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTAATATTTCAATAATATTGCTCACAAC 31
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                                                                                                                                                                                                                                                  Chow TP, Fry KE, Lim MY, Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 296; 402pp; English.
                                                                                                                                                                                                         (GENE-) GENELABS TECHNOLOGIES INC.
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                                                                                                     98WO-US008487
                                                                                                                                            97US-0045107P
97US-0061958P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.8%;
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Best Local Similarity 96.8'
                                                                                                                                                                                                                                                                                                                                                                            lasting immune response.
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                   WO9849314-A2
                                                                                                     25-APR-1998;
                                                                                                                                               25-APR-1997;
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                                                            05-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Helicobacter pylori antigens and related nucleic acid sequences -
useful in serological disgnosis and protective vaccines, providing long-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                   Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
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                                                                                                                                            Nucleotide sequence of clone Z14.ASM from cluster 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of cluster 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENELABS TECHNOLOGIES INC.
BP
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ID AAV90873 standard; DNA; 970 BP.
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Matches 30; Conservative
AAV90742 standard; DNA; 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori.
                                                                                                                                                                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                       WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                            25-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1997;
                                                                                20-MAR-2003
18-FEB-1999
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18-FEB-1999
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Query Match

AAV90873;

SXXXXXXXXXXXXX

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Gape

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1; Indels

Length 970;

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WO200277183-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang I
                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                               RESULT
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                                                                                  The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence represents a primer used to isolate polynucleotides encoding Helicobacter pylori proteins for studies on protein-protein interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes
                     complexes of protein-protein interactions in Helicobacter pylori, tul for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori DNA for cellular proliferation protein #135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick JD,
                                                                                                                                                                                                         81.9%; Score 25.4; DB 6; Length 30; 88.9%; Pred. No. 11; indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                     Sequence 30 BP; 10 A; 7 C; 1 G; 9 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ď,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 7318; 511pp; English.
                                                                                                                                                                                                                                                                 4 CUACUATTATTCAATAATATTGCTCAC 30
                                                                                                                                                                                                                                                   2 CTAATATTATTCAATAATATTGCTCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW,
                                                                Example 9; Page 561; 642pp; English.
                                                                                                                                                                                                                                                                                                                            AAS53681 standard; DNA; 1200 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
NOV-2000; 2000US-0255625P.
22-DEC-2000; 2000US-0255931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0191078P.
2000US-0206848P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001WO-US009180
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Xu HH;
                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
WPI; 2002-674910/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                            in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU35822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200170955-A2
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                    AAS53681;
                                 useful
                                                                                                                                                                                                                                                                                                          RESULT 7
AAS53681/c
                                                                                                                                                                                                                              Matches
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                           coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, beeudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for artibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
and the encoded proteins. The prokaryotes used are Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1200 BP; 365 A; 207 C; 319 G; 309 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1200; 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğξ,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1200 rrarrcaaraararrecreacaac 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TTATTCAATAATATTGCTCACAAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prokaryotic essential gene #16517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA34860 standard; DNA; 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ABU30990
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nucleic acid; (2) a nost cell containing the vector; (3) an isolated pulpapeptide or its fragment whose expression is inhibiting by the antisense nucleic acid; (4) an antibody capable of specifically binding callular prolypeptide; (5) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for che gene produce or that has an activity against a biological pathway required for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation or the biological pathway in which a proliferation-required gene or its gene product is one a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or owhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for dengined for proliferation in cells other than $S$. Typhimurium, $C$ of the grand genes of the present sequence is one of the target or cequired for proliferation in cells other than $S$. Typhimurium, $C$ or the printed specification, but was obtained in celectronic format directly from WIPO at $C$ or the present sequence and the coll of the printed pot sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1200 BP; 365 A; 207 C; 319 G; 309 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori polypeptide GHPO 750 3' DNA primer.
a host cell containing the vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.4%; Score 24; DB 100.0%; Pred. No. 34; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 TTATTCAATAATATTGCTCACAAC 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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1es 24; Conservative
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요
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Gaps

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Length 30; Indels

Score 21.6; DB 2; Pred. No. 2.4e+02; 0; Mismatches 4;

69.7%;

24; Conservative

Local Similarity

Query Match Matches 1 GCTAATATTATTCAATAATATTGCTCAC 28 GCTCGAGTTATTCAATAATATTGCTCAC 30

ð 요 ABN79830 standard; DNA; 2595

RESULT 10

ABN79830;

Seguence 30 BP; 8 A; 8 C; 4 G; 10 T; 0 U; 0 Other;

This 3' primer was used with a 5' primer (see AAV07967) in the PCR amplification of Helicobacter pylori strain ORV2001 genomic DNA in order to obtain DNA (see AAV07964) encoding a 50 kDa polypeptide (see AAW73035) designated GHPO 750. The primer pair includes a 5' clamp and BamHI and XhoI restriction enzyme reocgnition sequences for cloning purposes. The PCR product was ligated into vector pET28a, and recombinant polypeptide was expressed as a histidine-tagged fusion protein in E. coli host cells. The polypeptide can be used to develop vaccines for the treatment and prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct PI field.)

Example 3.B; Page 64; 184pp; English.

gastroduodenal diseases.

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Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metabolite by a fungua. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation the expression of at least one zinc binuclear cluster protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to improving the production of a secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 145; 49pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman A;
                                                                                                                                                                                                                                                       insecticide; antineoplastic; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maxon M,
                                                                                                                            Fungal ZBC gene sequence #67.
                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-2001; 2001WO-US029288.
                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-2000; 2000US-0233564P.
                                                                                        24-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holtzman D, Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROBIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-352005/38.
P-PSDB; ABP35641.
                                                                                                                                                                                                                                                                                                                               WO200224865-A2
                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002.
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New isolated Helicobacter polynuclectides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and

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Miller C, Algarawi

Tomb J,

Lissolo L,

WPI; 1998-568251/48. Kleanthous H,

(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC.

97US-00831310. 97US-00834666. 98WO-US006421.

> 01-APR-1997; 01-APR-1997;

Helicobacter pylori.

primer; 88. Synthetic WO9843479-A1

08-OCT-1998

31-MAR-1998;

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New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkabloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin, cell surface receptor; plant growth regulator; pigment; insecticide; antineoplastic; gene; ds.
an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling, a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a equivalent amounts of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the binass required for the production, which translates into decreased in records ABN794-ABN79911 represent ZBC genes of the sequences given in records ABN7974-ABN79911 represent ZBC genes of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to improving the production of a secondary metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholestrolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                      Query Match 67.7%; Score 21; DB 6; Length 2595; Best Local Similarity 82.8%; Pred. No. 3.8e+02; Matches 24; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                               Sequence 2595 BP; 829 A; 588 C; 491 G; 687 T; 0 U; 0 Other;
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as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, growth regulator, a modulator of cell surface receptor signalling, a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decreased in records ABN79764-ABN7911 represent ZBC genes of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pelet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present differentiating between healthy haematopoietic cells and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, comprises contacting a target nucleic acid with a reagent tl
distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, E
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                                                                                                                                                                                                                                                                                                  Length 2595;
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                                                                                                                                                                                                                                                                                                Score 21; DB 6; I
Pred. No. 3.8e+02;
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82.8%; Pred. No. s...
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                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                        Local Similarity
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Schwope I,
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ABZ10049/c
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ö related sequences and their complements, and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of hematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients ΰ Pelet Haematopoietic cell proliferation disorder related DNA seguence #335. lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SRPs) of haematopoietic cell proliferation disorder related sequences and their complements. Gape Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia, cytosine methylation state, gene, ds. Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piepenbrock C, Adorjan P, Grabs G, Leeche R, Leu E; Lewin A, Lipscher E, Maier S, Model P, Mueller V, Otto T, E Schwope I, Ziebarth H; haematopoietic cells; for differentiating between acute ; Sequence 5333 BP; 1248 A; 87 C; 1254 G; 2744 T; 0 U; 0 Other; DB 8; Length 5333; Score 21; DB B; Leus-Pred. No. 3.8e+02; 2983 CTAATATTATTAATAATATTATTCTTAA 2955 0; Mismatches 2 CTAATATTATTCAATAATATTGCTCACAA 30 ABZ10195/c ID ABZ10195 standard; DNA; 5333 BP 67.7%; 26-MAR-2002; 2002WO-EP003401. 26-MAR-2001, 2001US-0278333P. (first entry) Query Match 67.77 Best Local Similarity 82.87 Matches 24; Conservative (EPIG-) EPIGENOMICS AG WPI; 2003-018942/01. WO200277272-A2 Homo sapiens. 16-JAN-2003 03-OCT-2002 ABZ10195; 88888888888888888 유 ઠે

Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arreriosclerosis; anti-HIV; neuroprotective; antistrhitic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds; Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinuclectides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic classification of haematopoietic call proliferative disorders allowing for improved and informed treatment of patients disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; sa probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPS) of haematopoietic cell proliferation disorder Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle. Chemically pretreated genomic DNA associated with cell cycle #56 Sequence 5333 BP; 1248 A; 0 C; 1254 G; 2831 T; 0 U; 0 Other; Length 5333; Score 21; DB 8; Pred. No. 3.8e+02; 2983 CTAATATTATTAATAATAATATTATTCTTAA 2955 0; Mismatches 2 CTAATATTATTCAATAATATTGCTCACAA 30 Claim 1; SEQ ID NO 111; 28pp; English. Berlin K; ; 2000DE-01019058. ; 2000DE-01019173. ; 2000DE-01032529. ; 2000DE-01043826. 67.7%; 2000DE-01013847. AAS45406 Btandard; DNA; 8333 15-MAR-2001; 2001WO-EP002945 24; Conservative Piepenbrock C, WPI, 2001-602751/68. (EPIG-) EPIGENOMICS Local Similarity WO200168911-A2. Homo sapiens. 06-APR-2000; 07-APR-2000; 30-JUN-2000; 15-MAR-2000; 18-DEC-2001 20-SEP-2001 PCR primer AAS45406; Query Match Olek A, Matches AAS45406/ RESULT 88888888888888888 à 셤 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides. The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative Claim 28; SEQ ID NO 335; 117pp; English.

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                        of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for ediagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, asteriosclerosis, solid tumours and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiatitic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
genetic and/or epigenetic parameters for the diagnosis and therapy
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ABL33502 standard; DNA; 8333 BP.
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01-SEP-2000; 2000DE-01043826.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid relukaemia, Alzheimer's disease, Alzheilepsy, neurofibromatoaid rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention

Sequence 8333 BP; 1968 A; 183 C; 2037 G; 4145 T; 0 U; 0 Other;

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

Berlin

Piepenbrock C,

Olek A,

WPI; 2002-130909/17

(EPIG-) EPIGENOMICS AG.

Claim 1; SEQ ID NO 1475; 32pp + Sequence Listing; German.

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Score 21; DB 6; Lengtn esc. Pred. No. 3.8e+02;
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82.8%; Pred. No. s..
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Length 8333;

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ORGANISM: Human
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15466, A
15922, A
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14703, A
13635, A
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5265, Ap
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Sequence 13923, A
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                                                                                                  April 24, 2005, 00:51:24; Search time 60.2535 Seconds (without alignments) 841.853 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/Aa_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-14702
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                                                                                                                                                                                                                                                                                                      1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match
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US-09-04-016-13922/c

i Sequence 13922, Application US/09949016

i Patent No. 681239

i Fatent No. 681239

i Fatent No. 681239

i TITLE OF INVENTION:

I TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

I TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-10-414

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: FastESQ for Windows Version 4.0
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US-09-949-016-13923/c
Sequence 13923, Application US/09949016
Sequence 13923, Application US/09949016
Sequence 139239
GENERAL INFORMATION:
TATULE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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16137, A
16138, A
13358, A
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1199, Ap
1200, Ap
1197, Ap
1198, Ap
348, App
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170105,
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US-09-949-016-13353
US-09-949-016-60540
US-09-949-016-157403
US-09-949-016-157510
US-09-949-016-13504
US-09-949-016-13350
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US-09-949-016-13350
US-09-949-016-13350
US-09-949-016-1390
US-09-949-016-1390
US-09-949-016-1199
US-09-949-016-1199
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NAME/KEY: misc feature
LOCATION: (1) ... (278866)
OTHER INFORMATION: n = A,T,C or (US-09-949-016-13922
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Best Local Similarity 85.7%;
Matches 24; Conservative C
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Score 21.6; DB; Pred. No. 40; 0; Mismatches
                 CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEE OF WINDOWS Version 4.0
SSOFTWARE: 278866
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: misc_feature
| LOCATION: (1)...(278866)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13928
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Best Local Similarity 85.7<sup>3</sup>
Matches 24; Conservative
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Matches 24; Conservative
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; Sequence 13924, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOOU1307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PSELSEQ for Windows Version 4.0
; SEQ ID NO 13924
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
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                 PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILLING DATE: 2000-10-03
PRIOR PILLING DATE: 2000-10-03
PRIOR PILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 13923
LENGTH: 278866
                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LCCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13923
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; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13924
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ORGANISM: Human
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Length 278866; Indels

DB 4;

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Sequence 13926, Application US/09949016
; Sequence 13026, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VEWTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-00-10-03
; PRIOR PILING DATE: 2000-00-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PastSEQ for Windows Version 4.0
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85.7%; Pred. No. 40;
:ive 0; Mismatches
3 TAATATTATTCAATAATATTGCTCACAA 30
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US-09-949-016-14699/c
; Sequence 14699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION;
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LOCATION: (1).T.(278866)
OTHER INFORMATION: n = A,T,C or G
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-09

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14701

LENGTH: 278866
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85.7%; Pred. No. 40;
tive 0; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14701
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Best Local Similarity 85.7
Matches 24; Conservative
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Best Local Similarity
Matches 24; Conserv
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Sequence 14700, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERBENCE: CLOOD.1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOCTHAND APPLICATION NUMBER: (0/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOCTHAND APPLICATION NUMBER: 0/311,498

PRIOR PILING DATE: 2000-09-08

LENTHARE: FREEEE PREEEC FOR WINDOWS VERBION 4.0

SEQ ID NO 14700

LENTH: 278866
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 40;
0; Mismatches
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                                             FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 6/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 14699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

| LOCATION: (1)...(278866)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14699
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14700
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Best Local Similarity 85.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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US-09-949-016-14701/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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Gaps

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IndelB

Length 278866;

DB 4;

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-03
PRIOR PILING DATE: 2000-09-08
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65820 TAATATTATTCATTAAAATTTCTCAGAA 65793
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ilarity 85.7%; Pred. No. 40;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TAATATTATTCAATAATATTGCTCACAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14702
                                                                                                                    US-09-949-016-14702/c
; Sequence 14702, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
| LOCATION: (1)...(278866)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702
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; Sequence 14701, Application US/09949016

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US-10-101-464A-856
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                                                        GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-0-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 14703
LUMBER OF SEQ ID WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13635, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 13635
LENGTH: 94077
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Pred. No. 40;
0; Mismatches 4; Indels 0;
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Pred. No. 1.18+02;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65820 TAATATTATTCATTAAAATTTCTCAGAA 65793
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              Sequence 14703, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%;
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Best Local Similarity 85.7%;
Matches 24; Conservative
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Best Local Similarity 80.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
US-09-949-016-14703/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-13635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
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RESULT 12

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| Sequence 317, Application US/09422978 |
| Sequence 317, Application US/09422978 |
| Patent No. 6537751 |
| GENERAL INFORMATION: |
| APPLICANT: Cohea, Daniel |
| APPLICANT: Chumakov, 11ya |
| TITLE OF INVENTION: Blailelic markers for use in constructing a high density... |
| TITLE NEPRIENCE: GENNET.020CP1 |
| CURRENT PILING DATE: 1999-10-20 |
| EARLIER PPLICATION NUMBER: US 60/298,850 |
| EARLIER PPLICATION NUMBER: US 60/109,732 |
| EARLIER PILING DATE: 1998-11-23 |
| WUMBER OF SEQ ID NOS: 11796 |
| SEQ ID NO 317 |
| LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-101-4644-856

US-10-101-4644-856

Paquence 856 Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Collean M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling

FILE REFERENCE: 11000-10200-2

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1000-01-11

PRIOR FILING DATE: 1000-01-11

PRIOR FILING DATE: 1000-01-11

PRIOR FILING DATE: 1000-01-11

PRIOR FILING DATE: 1000-01-11
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 47;
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CCATION: 24
COTHER INFORMATION: 99-14186-424 : polymorphic base A or
US-09-422-978-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 20.2; DE; Pred. No. 90; 1; Mismatches
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Best Local Similarity 81.5%;
Matches 22; Conservative
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illarity 88.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 22; Conserv
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APPLICANT: VENTER.

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 00/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 15466
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Sequence 3, Application US/09693205A
; Patent No. 6812333
; GENERAL INFORMATION:
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Richter, Andrea C.
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REPERENCE: 2265. LO11-003
; CURRENT APPLICATION NUMBER: US 60/160,588
; PRIOR APPLICATION NUMBER: US 60/160,588
; NUMBER OF SEQ ID NOS: 73
; SOFURMER: SEASE OF OF Windows Version 4.0
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.5%; Score 20; DB 4; Length 43192; 82.1%; Pred. No. 1.5e+02; tive 0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 64.5%; Score 20; DB 4; Length 11492; Best Local Similarity ,82.1%; Pred. No. 1.4e+02; Matches 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S105 TAATATTTGCCATAATTTTTCTCACAA 5078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TAATATTATTCAATAATATTGCTCACAA 30
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Best Local Similarity 82.1;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
US-09-693-205A-3
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US-09-949-016-15466/c
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; ORGANISM: Human
US-09-949-016-15466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11492
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Search completed: April 24, 2005, 05:33:08 Job time : 70.4535 secs

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Sequence

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NGS-08-931-310-15
Sequence 15, Application US/08831310
Sequence 15, Application US/08831310
Sequence 15, Application Work of the sequence 15, Application No. US20020026035A1
SEQUENCE NO. NO. US20020026035A1
SETILE OF INVENTION: Helicobacter GHPO 1360 and TITLE OF INVENTION: Helicobacter GHPO 1360 and TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
     US-10-312-841-2
US-10-084-817-315
US-09-960-706-692
US-10-286-152A-5
US-10-286-152A-5
US-10-366-345-13
US-10-375-150-9
US-10-375-135-720-1327
US-10-062-674-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,175

REFERENCE/DOCKET NUMBER: 06132/037001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200

TELEFAK: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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113
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64.5 640681
64.5 640681
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87394
640681
                                                                                                                                            USA
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                                                                                                                             Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 7318, Ap
Sequence 7318, Ap
Sequence 22730, A
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                                                                                                      April 24, 2005, 02:04:39; Search time 250.62 Seconds (without alignments) 750.949 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-10-039-183A-17
1 US-08-831-310-3
1 US-10-662-126-32
1 US-09-815-242-7318
7 US-10-282-122A-22730
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                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               5633728 seqs, 3035525691 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-831-310-15
US-08-831-310-17
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Maximum Match 100%
Listing first 45 summaries
                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                         IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                       US-10-039-183A-15
                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
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Sequence 2, Appli Sequence 315, App Sequence 435, App Sequence 435, App Sequence 5, Appli Sequence 13, Appli

Sequence 3 Sequence 3 Sequence 3

Sequence 1, Sequence

sequence 189, App Sequence 135, App Sequence 1175, App Sequence 129, App Sequence 24648, A Sequence 27834, A Sequence 27834, A Sequence 166131, Sequence 166131, Sequence 22, Appl Sequence 317, Appl Sequence 3175, Appl Sequence 3175, Appl

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US-10-039-183A-15
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SENERAL INFORMATION:
SENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
TITLE OF INVENTION: GHPO 750 Polypeptides
TITLE OF INVENTION
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                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUERATING SYSTEM: DOS SOFTWARE: PASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/831,310 FILING DATE: 01-APR-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 06132/037001 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTAATATTATTCAATAATATTGCTCACAAC 31
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"Sequence 15, Application US/10039183A
; Publication No. US20030143242A1
; GENERAL INFORMATION:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-831-310-15
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
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STRANDEDNESS: single
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; APPLICANT: Kleanthous, Harold ; APPLICANT: Lissolo, Ling

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US-10-039-183A-17

Sequence 17, Application US/10039183A

Sequence 17, Application US/10039183A

Publication No. US20030143242A1

GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold

APPLICANT: Lissolo, Ling

APPLICANT: Tomb, Jean-Francois

APPLICANT: Miler, Charles

APPLICANT: Al-Garawi, Amal

TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules

TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules

FILE REFERENCE: 06132/037002

CURRENT APPLICATION NUMBER: US/10/039,183A

CURRENT APPLICATION NUMBER: US 08/831,310

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 31
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Publication No. US2020026035A1
Publication No. US2020026035A1
Publication No. US2020026035A1

APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEB: Clark & Elbing LLP
STREET: 176 Federal Street
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REFERENCE: 06132/037002
CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 08/031,310
PRIOR PLING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
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Pred. No. 0.19;
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100.0%; Score 31; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 31; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Helicobacter pylori
US-10-039-183A-17
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Best Local Similarity 100.'
Matches 31, Conservative
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Gaps

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Sequence 32, Application US/10662126

Sequence 32, Application US/10662126

Publication No. US20050063987A1

GENERAL INFORMATION:

APPLICANT: Hundt, Erika

APPLICANT: Hundt, Erika

APPLICANT: Schmidt, Karl-Heinz

APPLICANT: Schmidt, Karl-Heinz

APPLICANT: Schmidt, Karl-Heinz

TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use

FILE REPERENCE: CIR. OJ40

CURRENT APPLICATION NUMBER: US/10/662,126

CURRENT FILING DATE: 1999-012

PRIOR FILING DATE: 1999-012

PRIOR FILING DATE: 1999-012

PRIOR FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PATCHIN VOR: 2.1

SED ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
; LOCATION: (891)..(2090)
; OTHER INFORMATION: bp protein; 42 kD protein from Helicobacter pylori
US-10-662-126-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 2000-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/200, 848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/21, 578
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
Indels
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Pred. No. 0.36;
                                                                                                 1324 GCTAATATTATTCAATAATATTGCTCACAAC 1294
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                                                 1 GCTAATATTATTCAATAATATTGCTCACAAC 31
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 31; Conservative
  31; Conservative
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                                                                                                                                                                          RESULT 7
US-10-662-126-32/c
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  Matches
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APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Al-Garwa', Charles
APPLICANT: Al-Garwa', Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REPERENCE: 06132/037002
CURRENT FILING DATE: 2002-12-13
FRIOR PLING DATE: 1997-04-01
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Score 31; DB 8; Length 1448;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFBRATING SYSTEM: DOS
SOFTWARE: FASTERO FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILLING DATE: 01-APR.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAWE: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKEY NUMBER: 30,175
REFERENCE/DOCKEY NUMBER: 30,175
TELECOMMUICATION INFORMATION:
TELECHONE: 617-428-020
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Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 118...1314
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
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; LOCATION: (118)...(1314)
US-10-039-183A-3
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Best Local Similarity
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US-10-039-183A-3/C
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RESULT 10
US-08-831-310-8
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                                              Query Match
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-02-20
PRIOR PLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-28
PRIOR PLILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/206,335
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-09-06
PRIOR PLLING DATE: 2000-09-09
PRIOR PLLING DATE: 2000-09-09
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-24
PRIOR PLLING DATE: 2000-10-26
PRIOR PLLING DATE: 2001-02-09
PRIOR PLLING DATE: 2001-02-09
PRIOR PLLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-03
PRIOR PLING DA
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87;
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200 TTATTCAATAATATTGCTCACAAC 1177
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US-10-282-122A-22730/c
Sequence 22730, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Helicobacter pylori
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ...(1200)
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, LOCATION: (1)..
US-09-815-242-7318
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US-10-282-122A-22730

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Sequence 8, Application US/08831310
Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1160 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES: Clark Elbing LLP
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REFERENCE: 06132/037002
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                                               Gaps
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DB 17; Length 1200;
87;
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                                               Indels
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COPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: CLARK, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELECOMMULCATION INFORMATION:
TELEPHONE: 617-428-0200
77.4%; Score 24; DB 100.0%; Pred. No. 87; ive 0; Mismatches
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                                                                                            8 TTATTCAATAATATTGCTCACAAC 31
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                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Matches 24; Conserva
                       Best Local Similarity
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Query Match 67.7
Best Local Similarity 82.8
Matches 24; Conservative
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US-10-473-126-189/c
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  SEQ ID NO 145
LENGTH: 259
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yafhua
APPLICANT: Zhou, Yafhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 28120
LENGTH: 1290
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APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: 21nc Binuclear Cluster Proteins
FILE REFERENCE: 14184-019013
CURRENT PILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/29288
PRIOR FILING DATE: 2001-09-19
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Pred. No. 9.7e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                 Length 30;
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US-10-425-115-28120
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CURRENT APPLICATION NUMBER: US/10/039,183A CURRENT FILING DATE: 2002-12-13
    PRIOR APPLICATION NUMBER: US 08/831,310
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 30
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Publication No. US20040214272A1
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; Sequence 145, Application US/10149310

; Publication No. US20040077039A1
                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Helicobacter pylori
US-10-039-183A-8
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Best Local Similarity 82.8%;
Matches 24; Conservative
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GENERAL INFORMATION:

APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 189
LENGTH: 5333
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                                                                                                                                                                                                                                                                                                                                              Sequence 147, Application US/10149310

Publication No. US20040077039A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas

APPLICANT: Madden, Kevin T.

APPLICANT: Macon, Mary

TITLE OF INVENTION: Zinc Binuclear Cluster Proteins

FILE REFERENCE: 14184-019US1

CURRENT PLING DATE: 2003-02-19

PRIOR PLING DATE: 2001-09-19

PRIOR PLING DATE: 2000-09-19

PRIOR PLING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR PLING DATE: 2000-09-19

SOFTWARE: PatentIn version 3.1

SEQ ID NO 147

LENGTH 2595
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US-10-473-126-189
                                                                                                Score 21; DB 17; Length 2595; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 17; Length 2595;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 18; Length 5333;
Pred. No. 1.2e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Kluyveromyces marxianus var. lactis
US-10-149-310-147
                                                                                                                                                                                                                            1027 CTAATACTAAACAATAATATTACTCATAA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1027 craaracraacaaraararracrcaraa 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                             0; Mismatches
                                                                                                                                                                                            2 CTAATATTATTCAATAATATTGCTCACAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTAATATTATTCAATAATATTGCTCACAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 189, Application US/10473126
; Publication No. US20040234973A1
TYPE: DNA
CRGANISM: Kluyveromyces lactis
US-10-149-310-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%;
82.8%;
                                                                                              Query Match 67.7%;
Best Local Similarity 82.8%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.8°
Matches 24; Conservative
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Search completed: April 24, 2005, 05:52:17 Job time : 253.62 secs

BN10.020N BN15.027J BN15.027J OSIIEa03H CH261-120 MMB MMBCM 3591 1 6 CZIG03001 EST526371 EST526371 EST526371 EST526371 EST5670 MA CH210 MA CH210 MA CH210 MA CH210 MA CH210 MA

BES59176 H BP880225 C CD81234 D CD81287 B CD815821 B CC239056 C AG277970 M AG277970 M BD108331 E BD108331 E BD208331 E BD308331 E BD208331 E BD208331 E BD30831 E BD30831 E BD30831 E

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ALIGNMENTS
BES59176
BPR80225
CD812340
CD814287
CD815821
CC619111
CC239056
CC327685
CB170034
B1208597
CE024196
BF602438
BF602438
BF602438
BF602438
BF602439
BF70044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC266736 CH261-90B
AA516958 VAB5610.r
BH612485 SALK_0328
AG394257 Mus muscu
AG088415 Pan trog1
BX207173 Danio rer
AL381307 MEBC019B1
CR325923 Medicago
AL457517 T. brucei
AL457517 BCGWHBBD055
AL457636 Danio rer
AL61299 SP 0069 B
CC578276 TVEST09TB
CC114443 Shultzomi
AZ181814 SP 0175 A
BF065214 HV_CED0075
                                                                                                                                                              April 24, 2005, 00:31:54 ; Search time 1642.13 Seconds (without alignments) 718.576 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                              US-10-039-183A-15
31
1 gctaatattattcaataatattgctcacaac 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
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AL381307
AL381307
CR325923
TA68E10P
AQ49170B
BH433207
BH433207
BH2320328
BZ721736
CL010467
CL010467
CC010467
CC01047
CC01
                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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995-est2:::
995-est43::::
995-est44:::::
995-9881:::::
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                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                                      Run on:
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<u>₩</u> €	RESULT 1	
) ă	LOCUS	CC266736 958 bp DNA linear GSS 13-MAY-2003
1 Å	DEFINITION	B21 Sp6.1 CH261 Gallus gallus genomic clone
		genomic survey sequence.
Ă —	ACCESSION	
5	VERSION	CC266736.1 GI:30616030
2	KEYWORDS	GSS.
<u>ფ</u>	SOURCE	Gallus gallus (chicken)
	ORGANISM	Gallus gallus
•		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
		Phasianinae; Gallus.
2	REFERENCE	1 (bases 1 to 958)
	AUTHORS	Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
		Warren, W., Graves, T., Mardis, E. and Wilson, R.
	TITLE	Gallus gallus BAC End Reads
	JOURNAL	Unpublished (2003)
<u>დ</u>	COMMENT	Contact: Richard K. Wilson
_		Genome Sequencing Center
		Washington University School of Medicine
		Email: eubmissions@watson.wustl.edu
		Insert Length: 182000 Std Brror: 0.00
		oct process and control of the contr
		High mality semionge start. 7
		tituli distriction of the second of the seco
<u>.</u>	FEATURES	Location/Qualifiers
	source	1958
		/organism="Gallus gallus"
		/mol type="genomic DNA"
		/strain="Red Jungle Fowl"
		/db xref="taxon:9031"
		/clone="CH261-90B21"
		/sex="female"
		/cell line="UCD001, inbred 256"
		/clone lib="CH261"
		/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
		CH261 Female Chicken library - For library and clone
		ordering information: http://www.chori.org/bacpac"
-	ORIGIN	
	Query Match	76.1%;
	ыевт госа. Матлра	BESEL LOCAL SIMILISTICY B6./%; FIEG. NO. 1.96+UZ; Matches 26. Consequentive O. Mismatches 4. Indels O. Gans O.
	Haccince	כסופכו אמרז אל עודפווומרכווכם ז' זוותרום כלהם

1 GCTAATATTATTCAATAATATTGCTCACAA 30

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/mol_type="col-0"
/ectype="col-0"
/db_xref="taxon:3702"
/dlone="SALK 032806"
/clone="SALK 032806"
/clone="SALK 032806"
/clone="ECR was performed on Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dassel to 751)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan
(E-mail:hattoriegsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Clones are derived from the mouse BAC library MSWG01. For BAC
library availability, please contect Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG394257 751 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-213C16.TJ, genomic survey
                                                                   A (Dases 1 to 418)
A (Losses 1 to 418)
A (Losse, J. M., Losse, J.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDDA. This sequence lies within 300 bases of the 3' end of At3904770.
Class: TDNA tagged.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22.6; DB 8; Length 418;
Pred. No. 4.3e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                       Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies Tollo N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on/Qualifiers
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Mus musculus molossinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.9%;
                                                                                                                                                                                                                                                                                                                                                                        Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Locat
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Matches 25; Conserv
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
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                                                            REFERENCE
                                                                                  AUTHORS
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AG394257
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                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 550)
Marrah., Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                           EST 14-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                               AMADIGUSE EST 14-JUL-1 VM85410.rl Knowles Solter mouse E6 5d whole embryo Mus musculus CDNA clone IMAGE:893779 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:521739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, K.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Eax: 314 286 1810
Email: mouseest@watson.wustl.edu
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="embryo (post-implantation)"
/lab host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/db_xref="taxon:10090"
       197 AGTACTATTCAATAAAATTGCTCACAAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AATATTATTCAATAATATTGCTCACAAC 31
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Location/Qualifiers
1. .550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:893779
                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                     AA516958.1 GI:2256417
                                                                                                                                                                                                                                                                                                                                Mus musculus
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Best Local Similarity
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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KEYWORDS
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Gaps

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BX207173 589 bp DNA linear GSS 29-JAN-2003
Danio rerio genomic clone DKEY-234E10, genomic survey sequence.
BX207173
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This sequence was generated from the T7 end of BAC 234E10. 234E10 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
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MtBCO19B10F1 MtBC Medicago truncatula cDNA clone MtBC019B1 T3, mRNA
AL381307
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 589)
Humphray,S.J., Huckle,E. and Durham,J.L.
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                                           Length 1092;
                                         Score 22; DB 9; Length 109
Pred. No. 7.1e+02;
0; Mismatches 5; Indele
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92.0%; Pred. No. 8.4e+02;
tive 0; Mismatches 2;
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/tissue_type="Testis"
/note="vector pindigoBAC-536"
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/db xref="taxon:7955"
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Pan troglodytes DNA, clone: PTB-087F20.F, genomic survey sequence.
AG088415
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Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:sla1-45-503-9111, Fax:81-445-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                        /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                    'organism="Mus musculus molossinus"
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
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/organism="Pan troglodytes"
/mol type="genomic DNA"
/db xrefe"taxon:9598"
/clone="PTB-087F20.F"
                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-213C16.TJ"
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LOCATION/QUALIFIERB
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dev_stage="harvested 3 weeks post inoculation with Glomus
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Genoscope - Centre National de Sequencage
2 tue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégennoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Webbite:
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Peargol, V., and Gamas, P.
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                                                                                                                                                                                                                                                  http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Jemalong"
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'tissue_type="arbuscular
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Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db xref="taxon:3880"
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/tissue_Type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"
/clone_lib="mkDe"
/clone_lib="mkDe"
/clone_lib="mkDe"
/clone_Type="serilised seeds were germinated for 7h at 25 C, before transplanting into a 1/3 Epoisses soil: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LipA8). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks my was extracted from whole root systems. CDNA was prepared from polyah-enriched RNA. The cDNA was prepared from polyah-enriched RNA. The cDNA was directionally ligated into Unizap XR vector from Stratagene and packagin stracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
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Medicago truncatula
Medicago truncatula
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                   http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
                                                                                                                                                                                                                                                              'organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3880"
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TA68E10P/c DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT

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Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 580)
S Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
L Ontact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypansoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shorgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from '
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission
  Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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/clone="68f10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and mil@sanger.ac.uk and mil@sanger.ac.uk will Genomic DNA isolated from a cloned population of Rockville, WI Genomic DNA isolated from a cloned population of trypanosoma brucei (TRD27/4 GUTTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing A Practical Approach, eds. M. Vaudin and B.
/note="Vector: pindigoBAC ; Site 1: EcoRI ; Site 2: EcoRI ; Debelle F. and Chalhoub B.~Genoscope sequence ID : mtel-53L24RM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                              T. brucel sheared genomic DNA clone 68el0, forward sequence, genomic survey sequence.
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
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                                                                                                                                    69.7%; Score 21.6; DB 9; Length 524;
85.7%; Pred. No. 9.9e+02;
iive 0; Mismatches 4; Indels
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/organiam="Trypanosoma brucei"
/ol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                  218 TAATAATCTTCAATAATAATGCTCTCAA 245
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/clone="68e10"
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                                                                                                                                                                                          24; Conservative
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                                                                                                                                                                 Best Local Similarity
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RESULT 11 TA68F10P/c

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Best Loca Matches

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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GSS 24-APR-1999

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812 bp DNA linear GSS 18-WAR-2003 genomic survey sequence.
                                                            BZ503289 78 bp DNA linear GSS 16-DEC-2002 BONGE68TR BO 1.6 2 KB tot Brassica oleracea genomic clone BONGE68, genomic survey sequence.
                                                                                                                                                                                                             Brassica oleracea
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 782)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Wholbished (2001)
Other_GSSs; BONGE68TF
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1 (baes 1 to 832)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BONGES"
/clone liboNGES"
/clone lib="BO 1.6 2 KB tot"
/note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR Medical Center Drive, Rockville, MD 20850, USA. 171: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
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Pred. No. 1e+03;
0; Mismatches
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Unpublished (2003)
Other_GSSs: PUFGO46TD
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                                                                                                                                                BZ503289.1 GI:27021620
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Best Local Similarity 85.7%;
Matches 24; Conservative 0
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BZ820968
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BOGSW15TF BOGS Brassica oleracea genomic clone BOGSW15, genomic
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Brassica oleracea
Brusaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.

I (bases I to 70)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOGSW15TR
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                           / Bex. Male" (Call type="Lymphocytes" (Call type="Lympercil" (Calone lib="RPCI-11" (Calone libe"RPCI-11" (Calone "Vector: pBACe3.6; Site_1: EcoRI; RPCII1 Human Male BAC Library"
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
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Tel: 301-838-3523
Fax: 301-838-0208
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1. .580
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FEATURES

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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: Transport of the seq primer 
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Copyright (c) 1993 - 2005 Compugen Ltd.
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April 23, 2005, 10:03:10 ; Search time 177.401 Seconds (without alignments) 900.968 Million cell updates/sec 27 1 ggagaaatacaaatggcaaaagaaag US-10-039-183A-16 27 Title: Perfect score: OM nucleic Sequence: Run on:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003ds:* geneseqn2003cs: N_Geneseq_16Dec04:* geneseqn2001as:*geneseqn2001bs:* geneseqn2002as:*geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004as: geneseqn2004bs: geneseqn1990s:* geneseqn2000s:* geneseqn1980s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Aac37376 Arabidops Aac9510 Mouse fac Aav12115 Mus muscu Aav25812 Murine fa Aav31164 Mouse fac Adk48891 Wild type Aak73420 Human imm Aa199267 Human exc Aa453677 Human kid Ada71057 Rice gene Ada71057 Rice gene Ada71057 Rice gene Ada7351 Murine ca Ada73151 Murine ca Ada73160 Ada737 Rice gene Ada89095 Bacterial Adh84737 Entercocc Acc49506 Tumouras	Anf 58469 At CNGC1/D And 2452 Human dia Anf 58468 At CNGC1/D Anx 13047 Enterococ Abs 9842 Enterococ Continuation (4 of Acd 13446 Human DNA
AAC37376 AAC90510 AAV12115 AAV12115 AAX73164 AAX73420 AAX13420 AAX13420 AAX13420 AAX13420 AAX1057 AAX63629 ABD33351 AC495095 ACC49506 AAC649506 AAC649506	AAF58469 ACN42452 AAF58468 AAX13047 ABS98842 ABD32629_3 ACD13446
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ALIGNMENTS

GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR; Helicobacter pylori polypeptide GHPO 750 5' DNA primer. BP. 98WO-US006421. AAV07971 standard; DNA; 27 (revised)
(first entry) Helicobacter pylori. WO9843479-A1 31-MAR-1998; 25-MAR-2003 02-FEB-1999 08-OCT-1998. primer; ss. Synthetic. AAV07971; RESULT 1 AAV07971

(INWR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC. 97US-00831310. 97US-00834666. 01-APR-1997; 01-APR-1997;

Tomb J, Miller C, Lissolo L, Kleanthous H,

Algarawi A; WPI; 1998-568251/48. New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases. Claim 5; Page 156; 184pp; English. This 5' primer is used with a 3' primer (see AAV07972) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07964) encoding the a 50 kDa polypeptide (see AAW73035) designated GHPO 750. The isolated polynucleotide, and encoded

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antigen. (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DNA sequence codes for a 50 kDa Helicobacter pylori polypeptide (see AAW73035) designated GHPO 750. A polynucleotide encoding GHPO 750 can be obtained from genomic DNA by PCR amplification (see AAW73912-21 and invention provides polynucleotides (see AAW72001, AAV07912-21 and AAV07952-32), GHPO 750 and a 32 kDa Helicobacter polypeptides (see AAW7302-32), GHPO 750 and a 32 kDa polypeptide (see AAW73034). These polynucleotides were initially identified in a search of H. pylori genomic databases. DNA cassettes for expression of the Helicobacter proteins (unprocessed or mature forms) in prokaryotic or eukaryotic cells are provided. The polynucleotides can be used in vacciness to prevent or treat Hb infection in a mammal. Viral (especially poxvirus) or bacterial vectors are used. Products and methods of the invention allow treatment in prevention of gastroduodenal diseases associated with Hb infections, including acute, chronic, and atrophic gastritis, and peptic ulcer including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. Diagnostic and detection methods are also provided. GHPO 750 was demonstrated to be a protective
                                                                                                        ö
polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Helicobacter polymucleotides - used to develop products for
the diagnosis, prevention and treatment of Helicobacter infections and
gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                           GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis; therapy; ss.
                                                                                                        Gaps
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0
                                                                          100.0%; Score 27; DB 2; Length 27; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kleanthous H, Lissolo L, Tomb J, Miller C, Algarawi A;
                                                                                                                                                                                                                                                                                                                 Helicobacter pylori 50 kDa polypeptide GHPO 750 DNA.
                                                  Sequence 27 BP; 16 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                      1 GGAGAATACAATGGCAAAAGAAAG 27
                                                                                                                                1 GGAGAAATACAAATGGCAAAAGAAAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 150-152; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                         AAV07964 standard; DNA; 1448 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US006421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00831310.
97US-00834666.
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/*tag= a
                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                         Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-568251/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW73035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9843479-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                          25-MAR-2003
02-FEB-1999
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                                                                             Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27849
                                                                        ;
0
                              Score 27; DB 2; Length 1448;
Pred. No. 2.6;
Seguence 1448 BP; 466 A; 237 C; 364 G; 381 T; 0 U; 0 Other;
                                                                        Indels
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                 100.0%; Scor.
v 100.0%; Pred. No. 2...
'-- 0; Mismatches
                                                                                                                                      106 GGAGAATACAAATGGCAAAAGAAAG 132
                                                                                                            1 GGAGAAATACAAATGGCAAAAGAAAG 27
                                                                                                                                                                                                   RESULT 3
AAK73037/c
ID AAK73037 standard; DNA; 12834 BP.
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2000US-0216647P.
2000US-021680P.
2000US-0217487P.
2000US-0217496P.
2000US-0217496P.
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2000US-0225266P.
2000US-0225267P.
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2000US-0225270P.
2000US-0225447P.
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2000US-0189874P.
2000US-0190076P.
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2000US-0225759P.
2000US-0226279P.
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                                                                        27; Conservative
                                                       Local Similarity
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2000US-0231244P.
2000US-0231413P.
2000US-0231414P.
2000US-0232080P.
2000US-0232081P.
                                 1000US-0233065P
                                        000US-0234998P
                                                                                                                          2000US-0249214P
                                                                                             000US-02465
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient 's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients of host cell and culturing the cell to express the
cucies acids into a host cell and culturing the cell to express the
concerns and cancer metastesses of haematopoietic-aride cells. AAK67703
concerns and cancer metastesses of haematopoietic antigen genomic
sequences from the present invention. AAK879912 to AAK87950 and AAM82169
ceptesent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, SEQ ID NO 27849; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12834 BP; 3916 A; 2492 C; 2530 G; 3896 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 80.7%; Score 21.8; DB 4; Length 12834; Local Similarity 92.0%; Pred. No. 2e+02; nes 23; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGAGAAATACAAATGGCAAAAGAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC, Ruben SM,
                                 2000US - 0249217P
2000US - 0249218P
2000US - 0249244P
2000US - 0249245P
2000US - 0249265P
2000US - 024929P
2000US - 024929P
2000US - 024920P
2000US - 024920P
2000US - 024920P
2000US - 025929P
2000US - 025929P
2000US - 025929P
2000US - 025929P
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2000US-0251856P.
2000US-0251868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2001;
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Matches
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening defencing of bloactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for inhibiting the activity of CAP; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for inhibiting the effect of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (vii) for the carcinoma or a propensity to carcinoma; and (xi) for determing Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of
                                                                                                                                                                                                             Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82660 BP; 19374 A; 15352 C; 16570 G; 20443 T; 0 U; 10921 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.4; DB 11; Length 82660;
Pred. No. 3.1e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zagursky RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31339 ACATACAAATGGCAAAAGAAAG 31361
                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2017; Opp; English.
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                                                                                                                                                                                                                                      comprises a nucleotide sequence.
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ilarity 95.7%;
Conservative 0
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                      01-MAR-2002; 2002US-00087192.
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18-NOV-2002; 2002US-0426742P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH HOLDINGS CORP
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                                                                  (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                 WPI; 2003-328604/31.
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nes 22; Conserv
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                                                                                                                  Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB06507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to cancer-associated proteins (CAP) and the cancerassociated (CA) nucleic acids encoding them. The invention also relates to associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample of and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                          Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
Human cancer-associated (CA) gene HD07-048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243196 GGAGAATACAAATGGAAAAAAA 243172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse genomic sequence mCG9397.
                                                                                                                                                                                                                                                            15-DEC-2003; 2003WO-US040081.
                                                                                                                                                                                                                                                                                                              17-DEC-2002; 2002US-00322281.
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                                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Morris DW, Malandro MS;
                                                                       ds; cancer; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-499109/47.
                                                                                                                                                                 WO2004058146-A2.
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                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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80XCCCCCCCCCCCCX8X44X8XBXBXBXBXBXBXBXBXBXBXBXBXB

Best Loc Matches

ACN45192

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Gaps

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The present invention describes an isolated polymucleotide (I) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis as a Gram-positive bacterium. Also described:
C Alloiococcus otitidis as a Gram-positive bacterium. Also described:
C an isolated polypeptide that is encoded by the polymucleotide (I), its
c an isolated polypeptide that is encoded by the polymucleotide (I), its
complement, despenante variant or fragment; (3) a genetically engineered
those cell, transfected, transformed or infected with the vector of (2);
(4) an antibody specific for the polypeptide of (I); (5) an immunogenic
composition comprising the polypeptide, its complement, biological
equivalent or fragment, or the polymucleotide that is comprised in the
expression vector; (6) a pharmacoulical composition comprised in the
c expression vector; (6) a pharmacoulical composition comprised in the
c expression vector; (6) a pharmacoulical equivalent or fragment;
c of the polypeptides of (1), their biological equivalent or fragment;
c of the polypeptides of (1), their biological equivalent or fragment;
c ortificial in the biological sample; (10) a kit comprising an array
c of the antibody of (4); and (11) producing a polypeptide by culturing the
c ortificially enpiacered host cell under conditions suitable to produce the
c polymucleotides, polypeptides, antibodies and compositions of the present
c mortaning the novel polymucleotide, its degenerate variant or fragment,
c polymucleotides, polypeptides, antibodies and compositions of the present
c polymucleotides are useful for expressing and detecting Alloiococcus
c threating and monitoring of effects during drug clinical trials.

The polymucleotides are useful for expressing and detecting Alloiococcus
cottidis. The polymore encodes an Alloiococcus otitidis antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1200 BP; 343 A; 260 C; 264 G; 333 T; 0 U; 0 Other;
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                                                                                          Claim 7; SEQ ID NO 447; 1019pp; English.
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1754382
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effects during drug clinical trials.
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Best Local Similarity 88.55,
Local 23, Conservative
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Fragment Name
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ADB12064_08
ADB12064_09
ADB12064_10
ADB12064_11
ADB12064_12
ADB12064_13
ADB12064_13
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ADB12064_1
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from base 100001 (Allolococcus otitis entire genome JCCUS ADB12064 Accession Adb12064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated polymucleotide (1) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polymucleotide (1), (12) an expression vector comprising the novel isolated polymucleotide (1), (12) an expression vector comprising the novel isolated polymucleotide (1), (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (6) a pharmaceutical composition comprising the carrier; (7) a protein chip comprising the carrier; (6) a pharmaceutical composition comprising an array of the polypeptide of (1) and a carrier; (7) a protein chip comprising the comprision polypeptide of (1); their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus critidis in the biological sample; (10) a kit comprising a container containing the novel polymucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the collure. (1) can be used in gene therapy. The colypeptide from the culture. (1) can be used in gene therapy. The colypeptide from the culture. (1) can be used in gene therapy. The colypeptide sare useful for expressing and detecting Alloiococcus cultidis. The present sequence represents the entire genome of the process of the invention of the collider.
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                                                                                                                                                                                                                                                                                                                                                                                 New Alloiococcus otitidis polymucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
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  gene therapy; Gram-positive bacterium; infection; gene; ds.
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88.5%; Pred. No. 3.7e+02;
tive 0; Mismatches 3;
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18 fragments
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Best Local Similarity 88.5
Matches 23; Conservative
                                      Allotococcus otitis.
                                                                                                                                                                                                                                                                                                                                               WPI; 2003-505284/47.
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Continuation (2 of 18) of
WP Sequence split into 18
WP ADB12064_00
WP ADB12064_01
WP ADB12064_01
WP ADB12064_02
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                                                                              WO2003048304-A2
                                                                                                                                                                                                                                                                                                    Fletcher LD,
                                                                                                                      12-JUN-2003
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100001 200001 300001

Alloiococcus otitidis; antigenic protein; immunogenic; immunisation;

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2000US-0225470P.
2000US-0225447P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225681P.
2000US-022688P.
2000US-022882P.
2000US-0229343P.
2000US-0229343P.
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2000US-0231344P.
2000US-0231343P.
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2000US-0231343P.
2000US-023144P.
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2000US - 0232400P
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2000US - 023363P
2000US - 0233654P
2000US - 023365P
2000US - 0234274P
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2000US - 0239937P

2000US - 024128P

2000US - 0241785P

2000US - 0241804P

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2000US-0246524P.
2000US-0246524P.
2000US-0246525P.
                    14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
11-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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06-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
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08-SEP-2000;
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12-SEP-2000;
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08-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                           Score 21.2; DB 9; Length 110000;
Pred. No. 3.7e+02;
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88.5%; Pred. No. s...
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AAL37651/c
ID AAL37651 standard; DNA; 2004 BP.
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2000US-0186464P.
2000US-0186464P.
2000US-0189874P.
2000US-0199874P.
2000US-0199874P.
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2000US-0199874P.
2000US-0199874P.
2000US-0199874P.
2000US-019988P.
2000US-01488P.
2000US-011688P.
2000US-011749F.
2000US-01189P.
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2000US-0225266P.
2000US-0225267P.
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ADB12064_04
ADB12064_05
ADB12064_06
ADB12064_06
ADB12064_08
ADB12064_10
ADB12064_11
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14-AUG-2000;
14-AUG-2000;
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2000US-0249218P.
2000US-0249244P.
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2000US-0249264P.
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antifilammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                     Gapa
                                                                                                                                                                  Human musculoskeletal system related polynucleotide SEQ ID NO 4015.
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                     Indela
 4.3e+02;
; Score 20.8; DE; Pred. No. 4.3e+
                                                         855 GGAGAATACAAAGGACAAAAGAA 832
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                                       1 GGAGAAATACAAATGGCAAAAGAA
                                                                                               AAL37650/c
ID AAL37650 standard; DNA; 2004 BP
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2000US-0189874P.
2000US-01990076P.
2000US-0198123P.
2000US-0209467P.
2000US-0214886P.
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                     Conservative
           Similarity
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                                                                                                                                                                                                                                                          Homo sapiens.
Query Match
Best Local Simi:
Matches 22;
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                                                                                                                            AAL37650;
                                                                                       RESULT 10
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01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0231437P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-02313414P.
08-SEP-2000; 2000US-02313414P.
08-SEP-2000; 2000US-02313414P.
08-SEP-2000; 2000US-02313414P.
08-SEP-2000; 2000US-02313618P.
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2000US-0249208P.
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The invention relates to novel genes (AALJ4669-AALJ7666) and proteins (ABB00187-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Cronh's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, batent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
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ABX60638/c
ID ABX60638 standard; CDNA; 2004 BP.
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              2000US-0249216P.
2000US-0249214P.
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2000US-0249264P.
2000US-0249265P.
2000US-0249265P.
2000US-0249265P.
2000US-024929P.
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2000US-024929P.
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2000US-025039P.
2000US-025039P.
2000US-025039P.
2000US-025186P.
2000US-0251868P.
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10-DEC-2000; 2
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ABX60638

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08-DEC-2000; 2000US-0251868P
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08-DEC-2000;
20-OCT-2000;
01-NOV-2000;
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                             Gene; se; musculoskeletal system antigen; cancer; metastasis;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

wellovascular condition; wound; injury; burn; angiogenesis; ulcer;

well growth; telsue repair; limb regeneration; neuronal growth;

neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

AIDS-related complex; chondrocyte growth; bone regeneration;

periodontal regeneration; tissue transport; bone graft; skin aging;

well growth; hair loss; melanocyte growth; cell proliferation;

well growth; organ transplant; cell differentiation; body height; weight;

whair colour; skin; percentage of adipose tissue;

igmentation; commetic surgery; metabolism; blorythm; carlcadic rhythm;

depression; tendency for violence; pain; reproductive capability;

whormone level; endocrine level; appetite; libido; memory; stress;

storage capability; fat content; lipid content; protein content;

machigants.
                cDNA encoding novel human musculoskeletal system antigen #2982.
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                                                                                                                                                                               Homo sapiens.
26-FEB-2003
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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful CC for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid stimulates re-vascularisation of ischaemic tissues associated with conditions increats wounds due to injuries, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operation telimulates neuronal growth; can treat and prevent conditions, such as, Alzheimer's disease, parkinson's disease, and AIDS-conditions, such as Alzheimer's disease, Parkinson's disease, and AIDS-conditions, such as Alzheimer's disease, Parkinson's disease, and AIDS-conditions and periodontal regeneration and aid in tissue transports or bone grafts; prevents akin aging due to sunburn by stimulating cartivate hair-forming cells and promotes melanocyte growth; stimulates crowth prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates commaniation of hematopoietic cells and bone marrow cells chances tissue of mesodermal origin to differentiate in early embryonic stem cells, besides, haematopoietic lineage; modulates mammalian conference of adipose tissue, pigmentation, size, and shape (e.g., such as, body height, weight, hair colour, eye colour, chin, percentage of adipose tissue, pigmentation, size, and shape (e.g., shin, percentage of adipose tissue, pigmentation, size, and shape (e.g., shin, percentage or physical state by infiltunencing blooming chartes for physical state by infiltunencing blooming chartes for physical states by infiltunencing blooming chartes for confidencing controllers.
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                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding musculoskeletal system
associated polypeptides, useful for detecting disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 4015; 321pp; English.
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1es 22; Conservative
                                                                                                                                                                                                Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                WPI; 2003-128199/12.
                                                                                                BARASH S C.
(ROSE/) ROSEN C.A. (RUBE/) RUBEN S M.
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Matches
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Gene; se; musculoskeletal system antigen; cancer; metastasis;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-deformed condition; wound; injury; burn; angiogenesis; ulcer;

W post-operative tissue repair; limb regeneration; neuronal growth;

M post-related complex; chondrocyte growth; bone regeneration; disease;

M AIDS-related complex; chondrocyte growth; bone regeneration;

M reratinocyte growth; hair loss; melanocyte growth; cell proliferation;

W cell growth; organ transplant; cell differentiation; body height; weight;

M hair colour; eye colour; skin; percentage of adipose tissue;

M pigmentation; osmetic surgery; metabolism, blorhythm; caricadic rhythm;

depression; tendency for violence; pain; reproductive capability;

M hormone level; endocrine level; appetite; libido; memory; stress;

storage capability; fat content; lipid content; protein content;

Carbohydrate content; vitamin content; cofactor content;
            cDNA encoding novel human musculoskeletal system antigen #2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0217496P.
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                                                                                                                                                                                                                                             nutritional component
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                                                                                                                                                                                                                                                                        Homo sapiens.
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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastassa, in animals or humans. The nucleic acid; stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, and other cardiovascular conditions; and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal drowth; can treat and prevent neuronal damage occurring in certain disorders or neurodegeneration conditions, such as, Alzheimer's disease, Parkinson's disease, and AlDS-conditions, such as, Alzheimer's disease, Parkinson's disease, and AlDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or conditions, and all forming cells and promotes melanocyte growth, stimulates activate hair forming cells and promotes melanocyte growth, stimulates activate hair forming cells and promotes melanocyte growth, stimulates activate hair forming cells and promotes melanocyte growth, stimulates activate hair forming cells and promotes melanocyte growth, stimulates activate hair forming cells and promotes manualian organs before transplantation of for supporting cell culture of primary tissues; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian comments state by influencing biorhythms, caricadic rhythms, extension, tendency for violence, tolerance for pain, colour, eye copabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases tissue or decreases expanded to the protection of embory or stress; increases or decreases encodes a novel human musculoskeletal system components. This sequence encodes a novel human musculoskeletal system components. This sequence encodes a novel hum
                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2004 BP; 632 A; 428 C; 351 G; 593 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4016; 321pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 GGAGAATACAAAGGACAAAAGAA 832
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ID ADJ31388 standard; DNA; 2004 BP.
                  17-NOV-2000; 2000US-0249299P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
2000US-0244617P
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nes 22; Conservative
                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                      WPI; 2003-128199/12.
                                                                                                                                ROSEN C A.
RUBEN S M.
                                                                                                                                                                          (BARA/) BARASH S C
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2000US-02349979-
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08-NOV-2000;
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 musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
gene therapy; vaccine; human; ds.
Human musculoskeletal system-associated genomic DNA - SEQ ID 4015.
                                                                                                              2000US-0180628P.
2000US-0184664P.
2000US-0189536P.
2000US-0190076P.
2000US-019123P.
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2000US-0205467P.
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                                                       US2004009488-A1
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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14-SEP-2000;
                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated musculoskeletal system-associated nucleic acid molecule. The nucleic acid of the invention demonstrates cytostatic and osteopathic activities and may be useful for preparing a medicament for preventing, treating or ameliorating a medical condition such as cancer of the musculoskeletal tissues or osteoporosis, possibly via gene therapy or vaccine production. The current sequence is that of the human musculoskeletal system-associated genomic DNA of the invention. The current sequence is not shown within the specification per se but is available on the USPTO web-site
                                                                                                                                                                                                                                                           cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
gene therapy; vaccine; human; ds.
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                                                                                                                                                                                                                                     New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., G
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77.0%; Score 20.8; DB 12; Length 2004;
Best Local Similarity 91.7%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2004 BP; 629 A; 429 C; 353 G; 593 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 4015; 289pp; English
                                                                                                                                                                                                                                                                               musculoskeletal tissues or osteoporosis.
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2000US-0184664P.
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                    11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
17-JAN-2001; 2001US-00764877.
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2000US-0198123P.
2000US-0205515P.
08-DEC-2000; 2000US-0251990P.
                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                   Rosen CA, Ruben SM, Barash
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07-JUL-2000; 2000US-0216647P
07-JUL-2000; 2000US-0216880P.
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RESULT 14 ADJ31389/

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Score 20.8; DB 12; Length 2004; Pred. No. 4.3e+02;

77.0%; Scor. 91.7%; Pred. No. 4...

Query Match
Best Local Similarity 91."
Best Local Similarity 22, Conservative

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855 GGAGAATACAAAGGACAAAAGAA 832 GGAGAAATACAAATGGCAAAAGAA 24

Sequence 2004 BP; 632 A; 428 C; 351 G; 593 T; 0 U; 0 Other;

http:seqdata.uspto.gov/sequence.html?DocID=20040009488.

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Disclosure; SEQ ID NO 4016; 289pp; English.
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000; 2000US-0251479P.
000; 2000US-0251856P.
000; 2000US-0251868P.
000; 2000US-0251868P.
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000; 2000US-0251869P.
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                                                                                                                000US-0246610P
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                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-090458/09
                    08-NOV-2000;
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from base 100001 (Human chromosome: LOCUS AAD53224 Accession Aad53224 End
                                                                                                                                                                                                                                                                            Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                    1 GGAGAATACAAATGGCAAAAGAA 24
RESULT 15
ADD53224 1
CONTINUATION (2 Of 6) Of AAD53224 fr
WP Sequence split into 6 fragments
WP Fragment Name Begin
WP AAD53224 0
                                                                  fragments
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300001
400001
500001
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AAD53224_3
AAD53224_4
AAD53224_5
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associated nucleic acid molecule. The nucleic acid of the invention
demonstrates cytostatic and osteopathic activities and may be useful for
preparing a medicament for preventing, treating or ameliorating a medical
condition such as cancer of the musculoskeletal tissues or osteoporosis,
possibly via gene therapy or vaccine production. The current sequence is
that of the human musculoskeletal system-associated genomic DNA of the
invention. The current sequence is not shown within the specification per
se but is available on the USPTO web-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer of musculoskeletal tissues or osteoporosis.
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US-09-949-016-30717
   TYPE: DNA
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                                                                                                            April 24, 2005, 00:51:24; Search time 52.4789 Seconds (without alignments) 841.853 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30718,
Sequence 30719,
Sequence 87473,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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.: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
                  5.1.6
Compugen Ltd.
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US-09-949-016-87474
US-09-949-016-14206
US-09-949-016-12391
US-09-949-016-12391
US-09-249-016-12391
US-09-270-767-7990
US-09-270-767-7990
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-09-949-016-30719
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                  GenCore version
Copyright (c) 1993 - 2005
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seg length: 200000000
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Perfect score:
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US-09-449-016-30717/c

Sequence 30717, Application US/09949016

Patent No. 681239

THILE NO. F081239

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FABLES FABLES for Windows Version 4.0
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US-09-949-016-30718/c
; Sequence 30718, Application US/09949016
; Sequence 30718, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; CURRENT APPLICATION NUMBER: 06/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-3
; PRIOR PLING DATE: 2000-10-3
; PRIOR PLING DATE: 2000-10-3
; PRIOR APPLICATION NUMBER: 60/231,768
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Sequence 8
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Sequence 3
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US-09-949-016-166982
US-09-949-016-15648
US-09-949-016-11539
US-09-949-016-11720
US-09-949-016-11720
US-09-005-298-16
US-09-005-298-16
US-08-768-619-11
US-08-768-619-11
US-08-768-619-11
US-08-768-619-14
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Pred. No. 42;
0; Mismatches
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US-09-949-016-87475/c
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US-09-949-016-87475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87473
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; ORGANISM: Human
US-09-949-016-87474
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Sequence 87473, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PLIING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 87473

LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SEO ID NO 30719
LENGTH: 601
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30718
LENGTH: 601
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; Sequence 30719, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 88.5%;
Matches 23; Conservative (
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; ORGANISM: Human
US-09-949-016-30719
                                                                                                               TYPE: DNA
ORGANISM: Human
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USO-99-99-016-87474/c

1 Sequence 87414, Application US/09949016

2 Sequence 87414, Application US/09949016

3 Fatent No. 6812339

3 FALEANT: VENTER 100

4 APPLICANT: VENTER 100

5 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

7 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7 FILE REFERENCE: CL001307

7 CURRENT APPLICATION NUMBER: G0/241,755

PRIOR PELING DATE: 2000-10-20

7 PRIOR PELING DATE: 2000-10-03

7 PRIOR PELING DATE: 2000-09-08

7 PRIOR FILING DATE: 2001-03

7 PRIOR FILING
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Sequence 87475, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: FEBESEQ for Windows Version 4.0
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     Length 601;
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     DB 4;
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88.5%; Pred. No. 42;
ive 0; Mismatches
                                                                                               0; Mismatches
Score 21.2;
Pred. No. 42
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78.5%;
88.5%;
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Best Local Similarity 88.5
Matches 23; Conservative
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Sequence 1713. Application US/09949016

Sequence 1713. Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

FORMARE: PastSEQ for Windows Version 4.0
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Sequence 7990, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:
APPLICAMT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7990
                                           Length 109378;
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Pred. No. 1.1e+02;
0; Mismatches 2;
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                                                                                             0; Mismatches
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                                                Score 21.2;
Pred. No. 76;
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; ORGANISM: Drosophila melanogaster
US-09-270-767-7990
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Best Local Similarity 91.7%;
Matches 22; Conservative 0
                                           Query Match 78.5%;
Best Local Similarity 88.5%;
Matches 23; Conservative
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US-09-949-016-17103
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US-09-949-016-12391
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Sequence 12391, Application US/09949016

Patent No. 6812399

I PATENT NO. 6812399

I TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12391

LENTH: 109378
                                                                                                                                                                                                                            Sequence 14206, Application US/09949016

Sequence 14206, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTHARE: FREESE PRESE (for Windows Version 4.0

SEQ ID NO 14206
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                         3; Indels
Best Local Similarity 88.5%; Pred. No. 42; Matches 23; Conservative 0; Mismatches
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                                                                                                          192 GAAGATATACAAATGGCATAAGAAAA 167
                                                                       1 GGAGAAATACAAATGGCAAAAGAAAA 26
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14206
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LOCATION: (1)...(109378)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
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  Sequence 23272, Application US/09270767

Batent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburs et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 23272

LENGTH: 496
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Sequence 3258, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3258

LENGTH: 1381
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18540
LENGTH: 1381
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76.3%; Score 20.6; DB 4; Length 1381;
Best Local Similarity 85.2%; Pred. No. 78;
Matches 23; Conservative 0; Mismatches 4; Indels 0
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10S-09-270-67-18540/c
; Sequence 18540, Application US/09270767
; Patent No. 6703491
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; ORGANISM: Drosophila melanogaster
US-09-270-767-3258
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; ORGANISM: Drosophila melanogaster
US-09-270-767-23272
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; ORGANISM: Drosophila melanogaster
US-09-270-767-18540
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85.2%;
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Best Local Similarity
US-09-270-767-23272/c
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GENERAL INFORMATION:

Patent No. 6812339
GENERAL INFORMATION:
Patent No. 6812339
GENERAL INFORMATION:
PAPILICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-06
PRIOR PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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US-09-270-767-14658
US-09-270-767-14658
Sequence 14658, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburge et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REPRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14658
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Indels
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0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76908
                                              1 GGAGAAATACAAATGGCAAAAGAAAG 27
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US-09-270-767-14658
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milarity 95.5%; P
Conservative 0;
  23; Conservative
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US-09-949-016-76908
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Best Local Simil
Matches 21, C
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April 24, 2005, 02:04:39 ; Search time 218.282 Seconds (without alignments) 750.949 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
10: /ccn2_6/ptodata/1/pubpna/US10
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/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5633728 seqs, 3035525691 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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27
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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·	Sequence 16, Appl	Sequence 16, Appl	Sequence 3, Appli	Sequence 3, Appli	s 32, Appl	Sequence 5619, Ap	s 155136,	320, App	s 2017, Ap	s 61, Appl	Sequence 7892, Ap
Description	Sequence	Seguence	Sequence	Seguence	Sequence 32,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
αı	US-08-831-310-16	15 US-10-039-183A-16	US-08-831-310-3	US-10-039-183A-3	US-10-662-126-32	US-10-741-601-5619	US-10-425-115-155136	US-10-322-281-320	US-10-087-192-2017	US-10-331-053-61	US-10-674-124A-7892
DB	8	15	8	15	19	18	18	18	13	18	18
* Query Match Length DB ID	27	27	1448	1448		59914	522	256190	82660	83493	378
Query Match	100.0	100.0	100.0	100.0	100.0		82.2	80.7	79.3	79.3	78.5
Score	27	27	27	27	27	22.8	22.2	21.8	21.4	21.4	21.2
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INFORMATION FOR SEQ ID NO:

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	2		77.0			5-10-027-632-1702	e 1702
υ	14					-09-764-877-4	4015,
υ	15	20.8	77.0			US-09-764-877-4016	Sequence 4016, Ap
U	16		77.0	2004	17	US-10-242-515-4015	e 4015
υ	17		77.0	2004	17	US-10-242-515-4016	4016
	18		77.0	567564	18	US-10-699-156-3	Sequence 3, Appli
υ	19	20.6	76.3	668	13	US-10-027-632-12153	1215
U	20	20.6	76.3	668	11	US-10-027-632-12153	Sequence 121535,
υ	21	20.6	76.3	3463	13	US-10-027-632-258591	Sequence 258591,
υ	22	20.6	76.3	3463	11	US-10-027-632-25859	Sequence 258591,
υ	23	20.6	76.3	175590	10		Sequence 13, Appl
υ	24	20.6	76.3	175590	18		Seguence 13, Appl
	25	20.4	75.6	4526	13	Þ	Sequence 112, App
	26	20.4	75.6	1601042	13		Sequence 59064, A
	27	20.4	75.6	1601042	17	ns-	Sequence 59064, A
υ	28	20.2	74.8		13	₽	Sequence 221114,
U	29	20.2	74.8		11	US-10-027-632-22111	
υ	30	20.2	74.8		18		
	31	20.3	74.8		14	US-10-187-319-5	GENERAL INFORMA
	32	20.5	74.8		91	US-10-131-510A-5	Sequence 5, Appli
	33	20.2	74.8		18	US-10-491-464-5	Sequence 5, Appli
	34	20.2	74.8	7493	13	US-10-938-414-5	
	35	20.5	74.8		11	US-10-242-355-1031	Sequence 1031, Ap
υ	36	20.2	74.8			US-10-741-600-17689	
	37	19.8	73.3			US-10-437-963-77574	77574,
	38	19.8	73.3				Sequence 22395, A
	39	19.8	73.3	163	18	US-10-322-281-439	Sequence 439, App
	40	6	72.6		18	US-10-719-993-48777	48777
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	43	6	•		18	US-10-021-323-10810	10810,
υ	44	6			13	US-10-027-632-17060	Sequence 17060, A
υ	45	19.6		712	11	-10-027-632	17060,
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						ALIGNIENIS	
RESULT	LT 1						
us-o	8-831	US-08-831-310-16	,	4 1	,	(
. Se	quence blicat	ion No	ppiic US2	Sequence 16, Application US/08831310 Publication No. US20020026035A1	7086 35A1	31310	
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Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
APPLICANT: Kleanthous, Harold et al.
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES:
ANA STATE: MA
COUNTY: USA
COU
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RESULT 5
US-10-662-126-32
Sequence 32, Application US/10662126
; Publication No. US20050063987A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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Publication No. US20030143242A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Alesolo, Ling
APPLICANT: Alesolo
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08831310
Publication No. US20020026035A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
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                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 27; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 27; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IS COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
BAPLICATION NUMBER: US/08/831,310
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGAGAAATACAAATGGCAAAAGAAAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAGAAATACAAATGGCAAAAGAAAG 27
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ORGANISM: Helicobacter pylori
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLICY: linear
US-08-831-310-16
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COUNTRY:
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APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotide Molecules
FILE REPERENCE: 06132/037002
CURRENT APPLICATION NUMBER: US/10/039,183A
CURRENT APPLICATION NUMBER: US/10/039,1330
PRIOR FILING DATE: 1997-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 27; DB 8; Length 1448; 100.0%; Pred. No. 4.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06132/037001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10039183A; Publication No. US20030143242A1; GENERAL INFORMATION:
         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 0613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-020
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
LOCATION: 118...1314
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Genomic DNA
01-APR-1997
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (118)...(1314)
US-10-039-183A-3
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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Page 3

APLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 155136

LENGTH: 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 320, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 52945201000
CURRENT APPLICATION NUMBER: US/10/322,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: MOTHATION:
| APPLICANT: Engelhard, Eric K.
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
| TITLE OF INVENTION: CANCER
| FILE REFERENCE: 529452000122
| CURRENT FILING DATE: 2002-03-01
| PRIOR APPLICATION NUMBER: US 09/747,377
| PRIOR FILING DATE: 2000-12-22
| PRIOR APPLICATION NUMBER: US 09/7798,586
| PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.2%; Score 22.2; DB 18; Best Local Similarity 88.9%; Pred. No. 1.9e+02; Matches 24; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.8; DB 18;
Pred. No. 5.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: MRT4577_73066C.1
US-10-425-115-155136
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SOFTWARE: FastSEQ for Windows Version 4.0
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i OTHER INFORMATION: n = A,T,C or G
US-10-322-281-320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.0%;
Matches 23; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 256190
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US-10-087-192-2017
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| LOCATION: (1)...(59914)

| THER INDERVATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-741-601-5619
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                                                                                                                                                                                        APPLICANT: Knapp, Bernhard
APPLICANT: Hundt, Erika
APPLICANT: Hundt, Erika
APPLICANT: Hundt, Erika
TOTAL GENING: Mail-Heinz
TITLE OF INVENTION: Proteins, In Particular Membrane Proteins, of
TITLE OF INVENTION: Helicobacter Pylori, Their Preparation and Use
FILE REPERRORE: CHIR-0340
CURRENT APPLICATION NUMBER: US/10/662,126
CURRENT APPLICATION NUMBER: 09/230,158
PRIOR APPLICATION NUMBER: 09/230,158
PRIOR APPLICATION NUMBER: 09/230,158
PRIOR APPLICATION NUMBER: PCT/1E97/00981
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (891)..(2090)
OTHER INFORMATION: bp protein; 42 kD protein from Helicobacter pylori
US-10-662-126-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5619. Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CL001500
CURRENT APPLICAND NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FREETSEQ for Windows Version 4.0
SEQ ID NO 5619
LENGTH: 59914
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100.0%; Score 27; DB 19; Length 2825;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 27; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
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ORGANISM: Homo sapiens
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Best Local S:
Matches 24
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                                                                                                                                                                                                                                                                                          Score 21.4; DB 13; Length 82660;
Pred. No. 6.5e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3%; Score 21.4; DB 18; Length 83493; Best Local Similarity 95.7%; Pred. No. 6.5e+02; Matches 22; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 61, Application US/10331053
Publication No. US20040197778A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in Cancer FILE REFERENCE: 529452001100
CURRENT PILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 7892, Application US/10674124A
; Publication No. US2004019797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROS;
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: DOT/300/07621
; PRIOR APPLICATION NUMBER: DOT/300/07621
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-030
; PRIOR FILING DATE: 2000-0413
; PRIOR FILING DATE: 2000-0413
; PRIOR FILING DATE: 2000-0413
; PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2017
LENGTH: 82660
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                                                                                                                                                                     NAME/KEY: misc_feature; 10.0054100; 10.005410N: n = A,T,C or G
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LOCATION: (1)...(83493)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
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US-10-674-124A-7892/c
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LENGTH: 83493
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US-10-331-053-61
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OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 193304
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Sequence 17025, Application US/10027632

Bublication No. US20020198371A1

GENERAL INFORMATION:
APPLICATION
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Distance between a terminus base of telomere on OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base OTHER INFORMATION: sequence : 176502092 PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 4.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.8; DB 13;
Pred. No. 6.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                OTHER INFORMATION: chr4.fa.O7frz.184648907
PEATURE:
                                                                                                                                                                                                                                                                               OTHER INFORMATION: Located on chromosome 4 PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17025
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PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 7892
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Best Local Similarity 88.5%;
Matches 23; Conservative (
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Best Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-027-632-17025
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                                                                                                                                                    TYPE: DNA
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RESULT 13

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DB 9; Length 2004;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOS
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4016
LENGTH: 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
7e+02;
----- 2; Indels
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Pred. No. 7e+0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-4016
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                                                                            APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
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SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 17025
LENGTH: 699
   Sequence 17025, Application US/10027632
Publication No. US20030204075A9
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Best Local Similarity 91.74
Matches 22; Conservative
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US-10-027-632-17025
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Query Match 77.0%; Score 20.8; DB 9; Length 2004; Best Local Similarity 91.7%; Pred. No. 7e+02; Matches 22; Conservative 0; Mismatches 2; Indels 0

TYPE: DNA ORGANISM: Homo sapiens

SEQ ID NO 4015 LENGTH: 2004

US-09-764-877-4015

855 GGAGAATACAAAGGACAAAAGAA 832

Sequence 4016, Application US/09764877 Patent No. US20020147140A1

RESULT 15 US-09-764-877-4016/c

1 GGAGAAATACAAATGGCAAAAGAA 24

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GENERAL INCORMATION:
APPLICANT: Rosen et al.
TITLE DO INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PCOS
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0

36 GAAATAGAAATGGAAAAAGAAAG 59

Sequence 4015, Application US/09764877 Patent No. US20020147140A1

RESULT 14 US-09-764-877-4015/c

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/call_type="Spleen/Brain"
/clone_lib="RPCI-24"
/otche="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Wouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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CC727922 CGMAULSTV
CG009054 ZUACULSTV
CE522394 Ligr-gss-
AQ48881 RPCT-11-2
AL59036 VV04d03.x
AQ568710 HS 5319_B
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AZ99581 ZM028021
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AZ99581 ZM02802021
AZ99581 ZM02802021
AZ99581 ZM028701
                                                          April 24, 2005, 00:31:54 ; Search time 1430.24 Seconds (without alignments) 718.576 Million cell updates/sec
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        version 5.1.6
- 2005 Compugen Ltd.
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Listing first 45 summaries
                                          - nucleic search, using sw model
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AI593036
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bp DNA linear GSS 25-JAN-2001
musculus genomic clone RPCI-24-12004,
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Email: szkacoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 120 row: O column: 4
Seq primer: SP6
                                               PUPXM63TB
Mus muscu
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CM1-FT005
BY506979
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OR CBa009
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BX612579
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Labao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Mussell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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nab65f09.
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AGENCOURT
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                         CCF409277
CG463316
AG305267
BE964937
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CF283199
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Other GSSs: RPCI-24

Contact: Shaying Zhao

Department of Bukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
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1. 467
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CCF409276
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CCF40316
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AG305267
BE972541377
BE972541377
AW768154
AW768
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AW768154
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OGMAUISTH ZM 0.7_1.5_KB Zea mays genomic clone ZMWBMa0331C05, genomic survey sequence. CC727912
                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 727)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGNAU15TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD calde; Panicoideae; Andropogoneae; Zea.

1 (Daases 1 to 780)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Ocher GSSs: OGNAUISTY
Contact: Cathy Whitelaw
  OGMAU15TV ZM_0.7_1.5 KB Zea mays genomic clone ZMMBMa0331C05, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
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methylation filtered genomic_DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
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I (bases 1 to 567)

S Chao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0200

Fax: 301 838 02
                                                                                                                                                                                                                                                                                                                                                                                                      AQ488891 567NI.TV RPCI-11 Homo sapiens genomic clone RPCI-11-267NI, genomic survey sequence.
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BamH1 sites using MboI partially digested male C57BL/6J DNA."
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RPCII1 Human Male BAC Library"
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                                                                                                           Score 23.4; DB 8;
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                                                                                                           86.7%;
ilarity 96.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                  Query Match
Best Local Similarity
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CC727922/c
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AQ488891/c
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Gaps

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FEATURES

ORIGIN

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Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
CE522394 528-2693 525 bp DNA linear GSS 28-SEP-2003 tigr-ges-dog-17000365661989 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Eukaryota, Entamoebidae, Entamoeba.
E 1 (bases 1 to 907)
S Loffus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:MSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loffus
Contact: Brendan J Loffus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: blioftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
MNA library
Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                                   Bukaryota; Metracoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 525)
Kirkness; E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Frager, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     907 bp DNA linear GSS 14-DEC-200 STORIOGOTF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic gurvey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9615"
/clone_lib="hog_Library"
/note="Site_l: BatXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ekirknes@tigr.org
                                            genomic survey sequence
                                                                                         CE522394.1 GI:36839175
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/clone="xxwBpa0027D05"
/clone_lb="zm_3.0_4.0_KB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; PACCAD clade, Pandicoideae; Andropogoneae; Zea.

1 (bases 1 to 979)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: ZUACUISTV
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                           /.organism="zea maye"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="teaxon:4577"
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/clone="ZMMBMa0331C05"
/note="Woc="ZMMBMa0331C05"
/note="Woc="ZMMBMa0331C05"
/note="Woc="ZMMBMa0331C05"
methylation filtered genomic DNA library"
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84.4%; Score 22.8; DB 9; Length 780;
Best Local Similarity 92.3%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels
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84.4%; Score 22.8; DB 9; Length 979;
Best Local Similarity 92.3%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels
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9712 Medical Center Drive, Rockville, MD 20850, USA
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                     2 GAGAAATACAAATGGCAAAAGAAAG 27
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1. .979
/organism="Zea mays"
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG009054
CG009054.1 GI:33881220
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Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301-838-0208
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RESULT 5 CG009054 LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

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RESULT 6 CE522394

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GSS 14-DEC-2000

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Gaps

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AIS93036 396 bp mRNA linear EST 21-APR-1999 vv04d03.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1210661 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396)

Marray, M. Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R., Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
MGI:647005
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: polyT not found
High quality sequence stop: 385.
Location/Qualifiers
                                             /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3 6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1810

Fax: 314 286 1810
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Pred. No. 1.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                            Length 135;
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                                                                                                                                                                                         Score 21.8; DB 8;
Pred. No. 1.7e+03;
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/clone="IMAGE:1210661"
/sex="pooled"
clone="RPCI-11-267L9"
                                                                                                                                                                                                                                                                                          1 GGAGAAATACAAATGGCAAAAGAAA 25
                                                                                                                                                                                                                                                                                                                                108 GAAGAAGACAAATGGCAAAAGAAA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="NIH Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                       80.7%;
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Best Local Similarity 88.5%;
Matches 23; Conservative C
                      sex="Male"
                                                                                                                                                                                                                                            23; Conservative
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AI593036
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                                                                                                                                                             /db xref="taxon:5759"
/db xref="taxon:5759"
/db xref="taxon:5759"
/dlone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site="1" BET i; Constructed at The Institute for Genomic Research (TiGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, LiS.
CG, and Diamond, LiS. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(ppieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search/bac_end_search.html.
Seg primer: T7
Class: BAC ends.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
Uge of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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88.9%; Pred. No. 1.2e+03;
ive 0; Mismatches 3; Indels (
                                                                                                   'organism="Entamoeba histolytica"
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/db_xref="taxon:9606"
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strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGAGAAATACAAATGGCAAAAGAAAG 27
High quality sequence start: 15
High quality sequence stop: 853.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Other GSSs: RPCI-11-267L9.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .135
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Matches 24; Conservative
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REFERENCE AUTHORS

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RESULT 10 AQ568710/c LOCUS

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ABF--03-B23.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--03-B23, mRNA sequence.
                                                                                                                                                                                                                                                        Genoscope.
Direct Submission
Submitted (S-FEB-2004) Genoscope - Centre National de Sequencage : Submitted (S-FEB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Location/Qualifiers
                                                                       Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rogids; eurosids I; Pabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pIndigoBAC; Site_1: EcoRI; Site_2: EcoRI; Debelle F. and Chalhoub B.~Genoscope sequence ID: mtel-44M16RM1"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 298)
Xim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yorongli, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="leaf"
dev stege="14 days after germination"
/lab_host="8.coli blubs"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.7%; Score 21.8; DB 9; 92.0%; Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/mol type="genomic DNA"
/cultivar="Joanlong A17"
/db xref="taxon:380"
/clone_lib="MTE1"
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/cultivar="mRNA"
/db_xref="taxon:39947"
/clone="ABF--03-B23"
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                                                                                                                                                                                                            AQ568710 1590 bp DNA linear GSS 01-JUN-1999 HS_5319_B1_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=895 Col=23 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 590) Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone lib="RPCI-11 Human Male BAC Library"
//note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-38187
Emal: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Pred. No. 1.7e+03;
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'db_xref="taxon:9606"
                                                                             330 GGNGAATAAAATGGCAGAAGAAA 355
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.htsc.washington.edu
Plate: 895 row: B column: 23
Seq primer: T7
Class: BAC ends
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Homo sapiens
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Best Local Similarity 92.0
Matches 23; Conservative
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Khanna, A., Bolia, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Khanna, A., Bolia, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Rocann, R., Waterston, R. and Wilson, R.,

McCann, R., Waterston, R. and Wilson, R.,

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine

4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57066 USA (phone: 80 423 4163; email: info@biogeneticeervices.com)

Putative full length read vector to vector length is 551

Location/Qualifiers

Location/Qualifiers
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/organiam="Glycine max"
/mol_type="mRNA"
/culr_vaz="Bragg"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1081-3639"
/tissue_type="Roots of 7 day old 'Bragg' seedlings"
/tissue_type="Roots of 7 day old 'Bragg' seedlings"
/dew_stage="7 days old"
/dew_stage="7 days old"
/lone_lib="Gm-c1081"
/clone_lib="Gm-c1081"
/clone_lib="Gm-c1081"
/clone_lib="Gm-c1081"
/clone_lib="Gm-c1081"
/clone="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
XhoI; The mRNA was isolated from roots of 7 day old
'Bragg' seedlings that were mock-infected 48 hours prior
to harvest. Dr. Gary Stacey generously donated the
tissue. The roots were flash-frozen in liquid nitrogen.
Stratagene"s cDNA Synthesis Kit (catalog number 200401)
was used to synthesize the cDNA. First-strand synthesis
was performed with 5-methyl dCTP, hence the ligated cDNA
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8a097d08.y1 Gm-c1081 Glycine max cDNA clone SOYBEAN CLONE ID:

Gm-c1081-3639 5' similar to TR:Q40492 Q40492 CYCLIN A-LIKE PROTEIN.
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            /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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                                                                                                                                                                                                                              ch 78.5%; Score 21.2; DB 7; Length 298; 1. Similarity 88.5%; Pred. No. 2.7e+03; 23; Conservative 0; Mismatches 3; Indels
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CDNA library (ABF)"
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AUTHORS
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was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAACATGATCTCGAG[7]189] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the CDNA ends were filled in with cloned Pfu DNA, ligated to ECORI adapters and subsequently phosphorylated. The CDNA was then precipitated and redissolved in sterile, RNase-' DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by disgestion with XhoI from Promega (40U/ul); all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately Iml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with ECORI and XhoI, and phosphorylated by Stratagene's This Inbrary was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ814634 linear GSS 20-FEB-200
2M0082021F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone UUGC2M0082021 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Std Error: 0.00
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Insert Length: 10000 Std Error: 0
Plate: 0082 row: 0 column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 442.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GAGAAATACAAACAGCATAAGAAAAG 217
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .442
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/db_xref="taxon:10090"

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose golectrophoresis. Vector DNA was prepared from a derivative of pwalp (1732114 gbl A7129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Email: cpapbs-reparation: M. Bento Soares, Ph.D., cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 GGAGAATACAAATGGCCAATTAAAA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -400P from Gibco
High quality sequence stop: 417.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2417265"
clone="UUGC2M0082021"
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AI826431
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/lab_host="DH10B"
/clone lib="NCI CGAP Pr22"
/clone lib="NCI CGAP Pr22"
/note="Organ Prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; lst strand cDNA was prepared
with a modified polylinker; lst strand cDNA was primed with
a nor I - oligold() primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
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ORIGIN

Gaps ö ch 78.5%; Score 21.2; DB 1; Length 470; 1 Similarity 88.5%; Pred. No. 2.7e+03; 23; Conservative 0; Mismatches 3; Indels Best Local Similarity Query Match Matches

Search completed: April 24, 2005, 05:28:24 Job time : 1432.24 secs

THIS PAGE BLAMK (USPID)

OM nucleic

Run on:

Sequence:

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SM Mastadenovirus
Viruses, dsDNA viruses, no RNA stage; Adenoviridae.

Viruses; dsDNA viruses, no RNA stage; Adenoviridae.

E 1 (bases 1 to 27)

S Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.

76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polymucleotide molecules

L Patent: JP 2001523954-A 61 27-NOV-2001;

MERIEUX ORAVAX SOCIETE BN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC

PN JP 2001523954-A/61

PP 31-MAR-1998 JP 1998541962

PI HAROLD KLEANTHOUS, LING LISSOLO, JEAN PRANCOIS TOMB, CHARLES PI
AC005855 Mus muscu
AC019719 Drosophil
AC019871 Drosophil
AC06833 Homo sapi
AP002502 Homo sapi
AC06833 Homo sapi
AC002044 Drosophil
AC010815 Homo sapi
AC010815 Homo sapi
AC010359 Homo sapi
AC10359 Homo sapi
AC151502 Dasypus n
AC151544 Dasypus n
AC151944 Mus muscu
AC06805 Homo sapi
AC16605 Homo sapi
AC16632 Homo sapi
AC16633 Homo sapi
AC16633 Homo sapi
AC16633 Homo sapi
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AC122476 Mus muscu
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AC095632 Rattus no
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ADIN59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,A61K39/40,A61K39/40,G01N33/54,G01N33/569
Strandedness: Single;
Strandedness: Linear;
Foplogy: Linear;
Foplogy: Linear;
                                                                                                                                                                                                                                                                                                                                                                   27 bp DNA linear PAT 2 76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
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9
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    .27
    /organism="Mastadenovirus"
/mol_type="genomic DNA"
    /db_xref="taxon:10509"

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                                   AE008684_2
                                                                                                                                                                                 AC151944
AC068064
AC069272
AC146232
AC024283
AL158155
AC111065
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AE003584
AC100349
AC010350
AC108098
HS64K7
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Mastadenovirus
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Best Local Similarity 100.
Matches 27; Conservative
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172859
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AE0151939 Dasypus n
AC092647 Homo sapi
AC105330 Mus muscu
AC151655 Dasypus n
AC151656 Dasypus n
AC151564 Dasypus n
AC151566 Dasypus n
AC151566 Dasypus n
AC148072 Dasypus n
AC148072 Dasypus n
AC148073 Homo sapi
AC117393 Homo sapi
AC117393 Homo sapi
AC116215 Rattus no
AC116215 Rattus no
                                                                          April 23, 2005, 17:27:10 ; Search time 700.859 Seconds (without alignments) 1866.696 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                      4708233 segs, 24227607955 residues
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                1 ggagaaatacaaatggcaaaagaaag 27
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
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AC024886
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Gapop 10.0 , Gapext 1.0
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27
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seq length: 200000000
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86.7 163891
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Minimum DB Maximum DB

Database

Searched:

27-AUG-2002

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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

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AE000626 10532 bp DNA linear BCT 06-APR-1999
Helicobacter pylori 26695 section 104 of 134 of the complete
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Helicobacter pylori 26695
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Fleischman, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Bolton, R.C., Mackenbush, J., Zhou, L., Kirkness, E.F., Peterson, S., Loffus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.E., Gocayne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Karp, P.D., Smith, H.O., Fraser, C.M. and
PF 25-JUL-1997 JP 1998508651
PR 26-JUL-1996 DE 196 30 390.7
PR 26-JUL-1996 DE 196 30 390.7
PI BERNIARD KNAPP, ERIKA HUNDT, KARL HEINZ SCHMIDT PC
C12N15/31, C07K14/205, C07K16/12, G01N33/53, A61K31/70, A61K39/106, PC
A61K39/396
CC Strandedness: Single,
CC Strandedness: Single,
CC Topology: Linear;
Location/Qualifiers
FT Source 1.2825
FT Source /organism='Helicoharter'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 10532)
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Submitted (17-MAR-1999) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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/organism="Helicobacter pylori 26695"
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    .2825
    forganism="Helicobacter pylori"
|mol_type="genomic DNA"
|db_zref="taxon:210"

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Pred. No. 15;
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AE000626.1 GI:2314360
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Best Local Simil
Matches 27; C
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BD009865.1 GI:18638238
THElicobacter Pylori
SM Helicobacter pylori
Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
Helicobacteraceae; Helicobacter.
S Knapp, B., Hundt, E. and Schmidt, K.H.
S Knapp, B., Hundt, E. and Schmidt, K.H.
L. Peteins, in particular membrane proteins, of Helicobacter pylori, their preparation and use
CHIRON BEHING GMBH & CO
OS Helicobacter pylori
PN JP 2001502886-A 6
PD 06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                          SM Mastadenovirus
Viruses, dsDNA viruses, no RNA stage, Adenoviridae.

Viruses, dsDNA viruses, no RNA stage, Adenoviridae.

E 1 (bases I to 1448)

Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.

76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
corresponding polymuclectide molecules

L Patent: JP 200152394-A 54 27-NOV-2001;
MERIEUX ORAVAX SOCIETE BN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
HUMAN GENOME SCIENCES INC

PN JP 2001523954-A/54

PD 27-NOV-2001

PF 31-MAR-1998 JP 1998541962

PI HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES PI
                                                                                                                                                                                             BDDB2347
76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and corresponding polynucleotide molecules.
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Proteins, in particular membrane proteins, of Helicobacter pylori,
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A61K39/40,
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Pred. No. 16;

    .1448
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Strandedness: Single;
Topology: Linear;
Key
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                              Mastadenovirus
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PI AMP
PC AO
PC AC
PC G
CC S
CC F
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ORIGIN

FEATURES

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

DEFINITION

ACCESSION

RESULT 3 BD009865

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/gote="similar to SP:P42482 PID:587590 percent identity:
89.50; identified by sequence similarity; putative"
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/brotein id="AAD08250.1"
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ILVVSAADOPMPQTREBILLSRQVGVPHIVVELNKQDWVDDGELLELVBMEVLELSA
YEPGDDTPIVAGSALRALEEAKAGNVGEWGEKVLKLAAEVDAYIPTPERDTEKTPLM
PVEDVESIAGRGTVVTGRIBRGVVKVGDEBEUTGIRPTQKTTVTGVEMPTRELKGEA
GDWVGVLLAGTKKEEVERGWNLCKPGSITPHKKFEGEITVLSKEEGGGRATPPFTNWYPP

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IGHILEKMANRAAPKPKIFFEQGEVVRVVGGPFANFTATVEBYDVEHRKLKLNVSIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKVKIGLKCSDCEDINYSTTKNAKTNTEKLELKKFCPRENKHTL
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/db_xrefe="GI:2314365"
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complement(3354. .3512)
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/note="codon recognized: ACC"
complement (4982. .5055)
/gene="tRNA-Gly-2"
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complement(5186. .5258)
/gene="tRNA-Thr-2"
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                                                                                                                                                                                                                                                                               complement [3242. .3314)
/gene="tRNA-Trp-1"
complement (3242. .3314)
/gene="tRNA-Trp-1"
/product="tRNA-Trp"
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/product-"-
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/gene="tRNA-Tyr-1"
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/gene="tRNA-Thr-1"
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/gene="tRNA-Tyr-1"
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5448. .7184
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                                                                                                                                                                                                                                                                                                                                                                               /product="ribosomal protein L7/L12 (rpl7/l12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to SP:P42923 PID:786163 GB:AL009126 percent
identity: 30.38; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon start=1
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/product="ribosomal protein L10 (rpl10)"
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Valrigvodratadowykgavvlehgtgkkyravafakdikodeaknagadovyggddla
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Qvurrvdkkknyhatigkasppeekikenmlelvktiinrlkfssakgkyirnaalslt
Mspsvsldaqelmdik"
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TXDMOSFNIPVIITYYQDXEFFITKKPPVTDLIKKASGVEKGSDNPLKNKLAKLTH
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COMPLEMENT (2360. . 2890)
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GB:U00096 PID:1790414 percent identity: 41.04; identified
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                                                                                                                                                               complement (142. .519)
/gene="HP1199"
/note="Bimliar to SP:P05392 percent identity: 65.04;
/dentified by sequence similarity; putative"
/codon grart=1
/transI_table=11
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PID:1222450 PID:1204767 percent identity: 51.98;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P29395 GB:Z11839 PID:48184 GB:AE000512 percent identity: 63.83; identified sequence similarity; putative" /codon_start=1 /ranal_table=11
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protein id="AAD08247.1"
db_xref="GI:2314363"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1168. .1872)
/gene="HP1201"
'mol_type="genomic DNA"
'etrain="26695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1168. .1872)
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                                                                      db_xref="taxon:85962"
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/gene="HP1200"
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                                                                                                    complement (142, .519)
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/transl_table=11
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/producT="sLongarlon FacToR TU (EF-TU)"
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YEPRODTPIVAGSALRALEBAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTELM
PVEDVFSIAGRGTVVTGRIERGVVKVGDEVIVGTRATQKTTVTGVEMFKELEKGEA
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GDYVRTTDVTGSITLPEGVEMVMFGDNVKITVELISPVALELGTKFAIREGGRTVGAG
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FWSPNAFLSLLTEITVIVFFYSTLILTNWKITLVFTTILALQIFFIVKKVTVLIKKKG
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RYSIETVGFSLLILAVAYILFKYGEARMVLPTISMYALALYRILPSVTGVISYYNEIA
YNQLATNVYRSLSKTIVEBDLVPLDFNEKITLQNISFAYKSKHPVLAKNFNLTIQKGQ
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GIARALYDNPEILVLDBEATSALDNETESKIMDEIYQIAKNKTLIVIAHRLSTIERCEV
                                                                                                                                                  translation="MKVKIGLKCSDCEDINYSTTKNAKTNTEKLELKKFCPRENKHTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2365. .4101
/gene="jhp1129"
/note="Bimilar to H. pylori 26695 gene HP1206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4110. .4778)
/gene="jhp1130"
/note="shmilar to H. pylori 26695 gene HP1207"
/codon start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /noce="similar to H. pylori 26695 gene HP1208"
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complement(4966. .5955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4110. .4778)
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                                                                                                                                                                                                              complement (462, .1661)
codon_start=1
transl_table=11
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/gene="jhp1129"
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Helicobacter pylori J99
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Bacteria; Proteobacteria Epsilonproteobacteria; Campylobacterales;
I (base 1 to 15292)
Alm,R.A., Ling,L.S., Moir,D.T., King,B.L., Brown,E.D., Doig,P.C., Smith,D.R., Noonan,B., Guild,B.C., deJonge,B.L., Carmel,G., Tummino,P.J., Caruso,A., Uria-Nickelsen,M., Mills,D.M., Ives,C., Gibson,R., Merberg,D., Mills,S.D., Jiang,Q., Taylor,D.E.,
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|translation="MAKKKHKISTLKYFLRSLKQIYMLITFKEKMVFFLLVLMAVFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE001541 15292 bp DNA linear BCT 20-JAN-1999
Helicobacter pylori, strain J99 section 102 of 132 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori Nature 397 (6715), 176-180 (1999)
                      /note="similar to SP:P22618 PID:142020 percent identity: 26.18; identified by sequence similarity; putative" /codon start=1 /trans1 table=11 /product="multidrug resistance protein (hetA)"
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/note="similar to H. pylori 26695 gene HP1204"
                                                                                                                                                                                                                                                                                                    'Match 100.0%; Score 27; DB 1; Length 10532; Local Similarity 100.0%; Pred. No. 13; 0; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Helicobacter pylori J99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.astra-boston.com/hpylori)
Location/Qualifiers
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King, B.L., Alm, R.A. and Trust, T.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="rpmG"
/note="synonym: jhp1127"
complement(257. .415)
                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGAGAATACAAATGGCAAAAGAAAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA /strain="J99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:85963"
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Best Local 9
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FKKAVNKVISNDLEYYSFVLNONYIGNIQEIPNKEELINKINSVALKKGFIYSHZG
GSSRQYFSETNAQKIDAMRLKIEELKLSQNIDNHSYYFLLASLLESADKVANTASVYG
GRYKHLLINTIAAYTPFPKHFVSLNANEVYQDSNDLIGKISGDILYLDPPYNARQY
GANYHLLINTIAAYTPFTPKGKTDLPSYQKSSFCSRFOILNAFENLIKKARFKYIFLSY
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| db_xref="GI:4155725"
| translation="MAVVIKVVNGKIQEYENGNYKRTYDSNIVAADTDGHIVAAVTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLDLSYSLERVLQEDPARRKWEVILLYPGIHALLCYRLAHALH
KRRFYFIARALSQLARFITGIEIHPGAKIGRGLFIDHGMGVVJGETTEIGDDVTIYHG
VTLGGTGKFKGKRHPTLGNRVVVGAGAKVLGAICVGDDVRIGANAVVLSDLPTGSTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="MKFLALFFLALAGVAFAHDGGMGGMDM1KSYSILGAMIGLGIAA
FGGAIGMGNAAAATITGTARNPGVGGKLLTTWFVAMAMIEAQVIYTLVFAIIAIYSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MDFITINSGNRTEEFALKQVAKQATSSLMYRLGKTLILASVCVE
REPVSEDFLPLVVQFLEKSYAAGKIPGGFVKREGRAQDFEILTSRLIDRTLRPLFPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRY PTOITLMVLNHDI ENDLOVSALNAASATL FLAH I APIKSVSACRIARVDNEFIIN
PSASLLNOSSLDLFVSGTKESLNM I EMRSLGOKLNALEEPLMLEALELAOKSLKETCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product = "POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7507. .7602
'gene="jhp1134"
'note="similar to H. pylori 26695 gene HP1211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MVPKVGLEPTRDCSHQILSLACLPIPPLRRV"
complement (7804. .8121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to H. pylori 26695 gene HP1210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="similar to H. pylori 26695 gene HP1212"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="ATP synthase F0, subunit c"
protein id="AAD06717.1"
db_xref="GI:4155737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
/product="0-SERINE_ACETYLTRANSFERASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative"
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/db_xref="G1:4155736"
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/db_xref="G1:4155735"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: jhp1133"
complement(6692. .7207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: jhp1135"
complement(7804. .8121)
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/db_xref="GI:4155738"
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                                                                                                                                                                        complement (6284. .6463)
                                                                                                                                                                                                                                                                                                                                                                                  complement (6692. .7207)
/gene="cysE"
                                                                                                                                                                                              /gene="jhp1132"
/codon start=1
/transT_table=11
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transl_table=11
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LYEEAFTPYQNELLFKEGEGIVLNERLLDLLKNQYFDEIIKGIESSALSERENVPKEV
AKKISEAHSEPSLEEIELSLEKVKKTEIRRMIIQDKIRPDKRALEEVRPISIESNLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACISI939 113794 bp DNA linear HTG 13-OCT-2004 Dasypus novemcinctus clone VMRC5-357C17, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 8.18x in Q20 bases; agarose-fp
Quality coverage: 10.88x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 357C17

Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 113178 bases at least Q40
Consensus quality: 113375 bases at least Q30
Consensus quality: 11334 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 151000;
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                                                                                                                                                       Length 15292;
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8471: gap of unknown length
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HTG; HTGS PHASE1; HTGS DRAFT.
Dasypus nōvemcinctus (nine-banded armadillo)
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                                                                                                                                                 Query Match 100.0%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 12; Matches 27; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1673 GGAGAATACAATGGCAAAAGAAAA 1647
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Homo sapiens BAC clone RP11-419M24 from 7, complete sequence.
AC092647 AC027372
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Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 163891)
Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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L (bases 1 to 163891)
Sulston, J. E. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                               90.4%; Score 24.4; DB 2; Length 113794; 96.2%; Pred. No. 80;
                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:9361"
/clone="VNRCS-357C17"
/note="BAC resource: http://bacpac.chori.org/"
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Unpublished (2001)
3 (bases 1 to 163891)
Waterston,R.H.
2 51245: contig of 42774 bp in length 6 51345: gap of unknown length 6 113794: contig of 62449 bp in length. Location/Qualifiers
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                                                                                           organism="Dasypus novemcinctus"
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8472. 51245
/note="assembly_fragment"
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/note="assembly_fragment
clone_end:SP6
vector_side:left"
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Abbott,A. and VanBrunt,A.
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Waterston, R.H.
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                                                                           .113794
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see thttp://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                                                                            Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA ON Sep 104, 2001 this sequence version replaced gi:14916231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The clone sequenced to the left is RP11-613E4 the clone sequenced to the right is RP11-15K19. Actual start of this clone is at base position 1 of RP11-419M24 actual end is at base position 163891 of RP11-419M24.
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Data from AC091812 and AC092579 was used to finish this clone,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
Contact: Summary Statistics
Center: project name: H NH0419M24
Drafting Center: WIBR
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                                                                                                                            Wilson, R.
Direct Submission
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What musculus chromosome 15, clone KF23-Calcid
Unpublished

2 (bases 1 to 206675)

8 Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B.
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
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MacLean, C., MacGonald, P., Major, J., Marquis, N., Mathorin, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
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Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Viel, R., Yavers, M., Tavis, N., Travis, Travis, N., Travis, N., Travis, N., Tra
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Mus musculus chromosome 15, clone RP23-281C10, complete sequence.
AC105330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.7%; Score 23.4; DB 9; Length 163891; Best Local Similarity 96.0%; Pred. No. 1.7e+02; Matches 24; Conservative 0; Mismatches 1; Indels 0;
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Mus musculus
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AC105330/c
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ACCESSION
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KEYWORDS
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AUTHORS
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      Levine, "., "attoytate,", "standam,", "stand-regite, ", "falez,",", "hagosian, D., Hagosian, D., Hagosian, "., "thievine,", "lievine,", "Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., "Johnson,R., "Landers,T., Levine,R., "Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Manjor,J., Manning,J., Matthews,C., McCarthy,M., Weldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Micol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Romon,J., Schauer,S., Schupback,R., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seman,S., Severy,P., Senith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfayo,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Vonkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                 Submitted (26-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 26, 2004 this sequence version replaced gi:46358229. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
contect: sequence_submissions@broad.mit.edu
contect: Project_Information
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/rpt_family="(TCTA)n"
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477. .523
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Center clone name: 28
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Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R. W., Boakye, A., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Hanghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J. R., Madden, M., Maduro, Q.L., Marguilee, B. H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Park, M., Portnoy, M. B., Prasad, A., Puri, O., Reddix-Dugue, N., Rosas, B., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Stephen, E., Thomas, J. W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       118958 bp DNA linear HTG 22-SEP-2004
Dasypus novemcinctus clone VMRC5-394122, WORKING DRAFT SEQUENCE, 4
unordered pieces.
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Submitted (22-SEP-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Center project name: hth
Center clone name: 394122
Center clone name: 394122
Sequencing vector: plasmid; n/s; 100% of reads
Sequencing vector: plasmid; n/s; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 116712 bases at least Q40
Consensus quality: 116712 bases at least Q20
Insert size: 130000; agarose-fp
Insert size: 130600; agarose-fp
Coulity coverage: 9.64x in Q20 bases; sum-of-contigs
Quality coverage: 10.57x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                            Query Match 86.7%; Score 23.4; DB 10; Length 206675; Best Local Similarity 96.0%; Pred. No. 1.7e+02; Matches 24; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIS1655.1 GI:52421402
HTG: HTGS PHASEL; HTGS DRAFT.
Dasypus novemcinctus (nine-banded armadillo)
Dasypus novemcinctus
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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complement(21402. .22192)
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22205. .22234
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complement(22239. .22659)
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2 (bases 1 to 118958)
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AC151655
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ACISIGSS.1 GI:52421402
HTGS PHAGE1; HTGS DRAFT.
Dasypus novemcinctus (nine-banded armadillo)
Dasypus novemcinctus (nine-banded armadillo)
Dasypus novemcinctus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus.

I (bases 1 to 118958)
Antonellis, A. Ayele, K., Benjamin, B., Blakesley, R. W., Boakye, A., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Hangesh, N., Engle, J., Hu, P., Hurle, B., Idol, J. R., Jones, C., Kwong, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Madden, M., Maduro, O.L., Mangeulies, E.H., Mastello, C., Maskeri, B., McDowell, J., Mullkin, J.C., Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Duque, N., Rosas, B., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantitop, S., Stephen, E., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.

Unpublished
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Submitted (22-SEP-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                      5516: contig of 5516 bp in length
5616: gap of unknown length
2625: contig of 20909 bp in length
26625: gap of unknown length
73518: contig of 46893 bp in length
73618: gap of unknown length
118958: contig of 45340 bp in length.
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26626. .73518
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5617. 726525
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                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 116712 bases at least Q30
Consensus quality: 116712 bases at least Q30
Consensus quality: 116712 bases at least Q30
Insert size: 130000; agarose-fp
Insert size: 130608; sum-of-contigs
Quality coverage: 9.64x in Q20 bases; sum-of-contigs
Quality coverage: 10.57x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5516: contig of 5516 bp in length
517 5615: gap of unknown length
617 26525: contig of 20909 bp in length
526 26625: gap of unknown length
626 73518: contig of 46893 bp in length
519 73618: gap of unknown length
629 118958: contig of 45340 bp in length.
620 Location/Qualifiers
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ACISIS64.
ACISIS64.1 GI:52077673
HTG; HTGS_PHASE1; HTGS_DRAFT.
BASYPUS novemcinctus (nine-banded armadillo)
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mol_type="genomic DNA"
db_xref="taxon:9361"
                  Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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                                                                                                                     ----- Summary Statistics
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clone_end:SP6
vector_side:right"
5617. .26525
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/note="assembly_fragment
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                                                                             Center project name: hth
Center clone name: 394122
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AC151564/c
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RATTIONS

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us-10-039-183a-16.rge

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**NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**All 6230 contig of 6130 bp in length 6231 16395: contig of 10705 bp in length 6231 16395: contig of 10705 bp in length 17036 24333: contig of 1298 bp in length 17036 24333: contig of 1298 bp in length 17036 24333: contig of 10345 bp in length 17036 24334: gap of unknown length 189534 49978: contig of 10345 bp in length 18979 55079: gap of unknown length 18979 55079: gap of unknown length 18079 53148: contig of 3845 bp in length 18079 55149 57033: contig of 3845 bp in length 18779 61059: gap of unknown length 18779 57033: contig of 4476 bp in length 18779 57033: contig of 4476 bp in length 18779 61659: contig of 4476 bp in length 18770 61705: gap of unknown length 187703: contig of 1845 bp in length 187703: contig of 1845 bp in length 187703: contig of 18470 bp in length 187703: contig of 1
gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 139461 bases at least Q40
Consensus quality: 140443 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 141289; sum-of-contigs
Quality coverage: 15.19x in Q20 bases; sum-of-contigs
Quality coverage: 16.66x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 90830: contig of 28961 bp in length
31 90830: gap of unknown length
31 142189: contig of 51359 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Dasypus novemcinctus"
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6231. 16935
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'note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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AC148072.

AC148072.

AC148072.2 GI:46409669

HTGS PHASE2: HTGS DRAFT.

Dasypus novemcinctus (nine-banded armadillo)

Dasypus novemcinctus (nine-banded armadillo)

Bukeryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus.

E 1 (bases 1 to 142189)

Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,

Bouffard,G.G., Brinklay,C., Brooks,S., Chu,G., Coleman,B.,

Coleman,H., Daki,N., Engle,J., Garnite,S., Guan,X., Gupta,J.,

Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B.,

Idol,J.R., Jones,C., Karlins,E., Kim,H., Kwong,P., Laric,P.,

Larson,S., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,

Margulles,B.H., Masiello,C., Maskeri,B., McDowell,J.,

Mullikin,J.C., Paguirigan,C., Portnoy,M.E., Prasad,A., Puri,O.,

Reddax-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C.,

Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L.,

Wetherby,K.D., Young,A. and Green,E.D.

NISC Comparative Sequencing Initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-JAN-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 142189)
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                                                                                                                                                                                                                                                                                                                               Query Match 84.4%; Score 22.8; DB 2; Length 138155; Best Local Similarity 92.3%; Pred. No. 2.8e+02; Matches 24; Conservative 0; Mismatches 2; Indels 0;
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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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clone_end:SP6
vector side:left"
(8591...138155
/note="assembly_fragment
clone_end:T7
vector_side:left"
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Center clone name: 408P13
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                                                                                                                   misc_feature
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

VERSION KEYWORDS SOURCE ORGANISM

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LOCUS RESULT 12 AC148072

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Center: NIH Intramural Sequencing Center
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AUTHORS
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TITLE
JOURNAL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus.

1 (bases 1 to 148254)

Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Boakye, A.,

Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Daki, N.,

Engle, J., Guan, X., Gupta, J., Hanghighi, P., Han, J., Hansen, N.,

Ho, S.-L., Hu, P., Hurle, B., Idol, J. R., Jones, C., Kwong, P., Laric, P.,

Larson, S., Lee-Lin, S.-Q., Legaspi, R., Madden, M., Maduro, Q.L.,

Mullikin, J. C., Park, M., Portnoy, M. B., Prasad, A., Puri, O.,

Reddix-Dugue, N., Rosas, B., Schandler, K., Schueler, M. G., Shah, K.,

Sison, C., Stantripop, S., Stephen, B., Thomas, J.W., Thomas, P.J.,

Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, B.D.

Unpublished
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                                                                                                                                                                                                                                                                                                                               ACL51566 148254 bp DNA linear HTG 15-SEP-200
Dasypus novemcinctus clone VMRC5-53603, WORKING DRAFT SEQUENCE, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-SEP-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
Grovemont Circle Genome Center
Center: NIH Intramural Sequencing Center
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 146305 bases at least Q30
Consensus quality: 147095 bases at least Q30
Consensus quality: 147095 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 147954; sum-of-contigs
Quality coverage: 9.02x in Q20 bases; sum-of-contigs
Quality coverage: 10.24x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                Length 142189;
                                                                                                                                           ö
                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7425: contig of 7425 bp in length 7525: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                             AC151566.1 GI:52077675
HTG, HTGS PHASEL; HTGS DRAPT.
Dasypus novemcinctus (nine-banded armadillo)
Dasypus novemcinctus
                                                                                        84.4%; Score 22.8; DB 2;
92.3%; Pred. No. 2.8e+02;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                104270 GGAGAAATACAAATGGCTAAAAAAAA 104295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: hsz
Center clone name: 536003
------ Summary Statistics
                                                                                                                                                                                        1 GGAGAAATACAAATGGCAAAAGAAAA 26
clone_end:T7
vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 148254)
                                                                                                                                           24; Conservative
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green, E.D.
                                                                                                                                                                                                                                                                                                         RESULT 13
AC151566/c
                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                  ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Dasypodidae; Dasypus.

Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bulfard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Daki, N., Engle, J., Granies, S., Guan, X., Gupta, J., Han, J., Han, M., Malen, M., Maduro, Q.L., Maduro, Q.L., Maduro, W.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Portnoy, M.B., Praead, A., Puri, O., Redix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
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Dasypus novemcinctus clone VMRC5-308A3, WORKING DRAFT SEQUENCE, 15
ordered_pieces.
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Submitted (06-MAY-2004) NIH Intramural Sequencing Center, 8717

Grovemont Circle, Gaithersburg, MD 20877, USA

On May 6, 2004 this sequence version replaced gi:45736662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
7526 17697: contig of 10172 bp in length
7698 17797: gap of unknown length
7798 70396: contig of 52599 bp in length
7798 70496: gap of unknown length
7798 148254: contig of 77788 bp in length
7798 7148254: contig of 77788 bp in length
7778 bp in length
7778 bp in length
7778 bp in length
7788 bp in 
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HTG; HTGS PHASE2; HTGS DRAFT.
Dasypus novemcinctus (nine-banded armadillo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.4%; Score 22.8; DB 2; 92.3%; Pred. No. 2.8e+02; tive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment
clone end:T7
vector_side:left"
7526. .17697
/note="assembly_fragment"
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/note="assembly_fragment"
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Best Local Similarity 92.3
Matches 24; Conservative
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross missasemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  **NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

$55 contig of 856 bp in length $55 contig of 856 bp in length $55 contig of 17797 bp in length $55 contig of 11350 bp in length $1874 18853; gap of unknown length $10204 30203; contig of 11350 bp in length $10304 33073; contig of 2770 bp in length $1374 46563; contig of 2770 bp in length $4564 46663; gap of unknown length $4565 contig of 7050 bp in length $5656; gap of unknown length $5655; gap of unknown length $5656; gap of unknown length 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 162523 bases at least Q40 Consensus quality: 162523 bases at least Q30 Consensus quality: 163115 bases at least Q20 Insert size: 172000; agarose-fp Insert size: 163478; sum-of-contigs Quality coverage: 8.87x in Q20 bases; sum-of-contigs Quality coverage: 9.33x in Q20 bases; sum-of-contigs
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gap of unknown length
contig of 10731 bp in length
gap of unknown length
contig of 25917 bp in length.
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gap of unknown length
contig of 11152 bp in length
gap of unknown length
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gap of unknown length
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contig of 3017 bp in length
gap of unknown length
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gap of unknown length
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1. .164878
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/mol_type="genomic DNA"
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
------- project Information
                                                                                                                                                                     Center project name: gan
Center clone name: 308A03
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93350
93450
96467
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FEATURES Source

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (Dases I to 173270)

B. (Dases I to 173270)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bindse, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M. Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Chowdhry, I., Chistopoulos, C., Cleveland, C.D., Cox, C., Chow, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Dapaper, H., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Dapaper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
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Homo sapiens 3 BAC RPI1-25K24 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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/clone_lib="VMRC5"
/note="BAC resource: http://bacpac.chori.org/"
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                                                                                                                                                                                                                                                                                                                               49807. .56856 /note="assembly_fragment" 56957. .79408 /note="assembly_fragment"
                                                                                                                                                                                                                                                13174. .46563
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                                                                                                                                                                                                       10304. .33073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_fragment"
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138962. .164878
                                          .. .856
/note="aggembly_fragment
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                                                                                                    vector side:left"
957. .18753
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                                                                                     clone end:SP6
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Best Local Similarity
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AUTHORS
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Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Gazer,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Gazer,M., Gall,R., Gorrell,J.H., Guevara,W., Gunarathe,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hallows,C., Hollins,B., Homei,F., Howard,S., Huber,J., Hulbr,J., Lidolan,E., Karlson,E., Kally,S., Khan,U., King,L., Korvah,J., Kovar,C., Karlson,E., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,R., Martindale,A., Martinez,E., Massey,E., Martin,R., Martindale,A., Martinez,E., Massey,E., Martin,R., Martindale,A., Martinez,E., Mosten,M., Moncish,T., Morris,S., Moser,M., Nal,D., Nelson,D., Newtson,Y., Newtson,N., Nguyen,N., Nguyen
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Worley, K.C.

Direct Submission

Submitted (27-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 1, 2001 His sequence version replaced gi:16519437.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Direct Submission
Submitted (02-MAR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
1 (bases 1 to 173270)
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Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Havlor Plaza, Houston, TX 77030, USA
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4 (bases 1 to 173270)
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Unpublished
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AUTHORS
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

ANNOTATION OF FEATURES:

Features listing.

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                   QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                         http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2066 of clone AC117454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function="clone overlap"
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1708. .11761
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complement(11847..12113)
/rpt_family="LimC5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1. .2066)
/note="overlaps bases 1.
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complement(5596. .2721)
/rpt_family="AluSq/x"
2722. .2897
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/rpt family="MIR"
complement(8972. .9105)
/rpt family="L2"
10672. .11018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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8285. .8320
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complement (8489. .8520)
/rpt_family="L2"
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1209. .1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DN/
/db_xref="taxon:9606"
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/rpt_family="(CATA)n"
8380. .8400
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11333. .11418
/rpt_family="LIMB7"
complement (11419. .1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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476. .4950
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145...7190
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complement(4002.
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84.4%; Score 22.8; DB 9; Length 173270;
Best Local Similarity 92.3%; Pred. No. 2.78+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0;
      rpt family="Alusx"
omplement (24365. .24651)
rpt_family="Aluy"
                                                                                                                                                                                rpt family="AluSq"
omplement (22172. .22439)
rpt family="AluJo"
3743. .24050
                                                                                                                                                                                                                                                                    rpt family="MER5A"
complement(25417, .25595)
rpt family="MER5A"
5605, .25773
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25838. 25906
/rpt_family="MIR"
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Search completed: April 24, 2005, 03:21:54 Job time : 704.859 secs

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AJ548667 Trypanoso CL032403 CH216-34H CL168109 104-318_1 CL168109 104-318_1 BJ370495 BB425780 BJ370495 BJ370495 AM897234 CM0-NN005 BY453219 BY453219 AM897234 CM0-NN005 BY653219 BY453219 AM897234 CM0-NN005 BY653219 BY65212. CL876916 abf15c12. CL876916 abf15c12. CL876916 abf15c12. CL876916 abf15c12. CL876916 abf15c12. CL876914 abf15c12. CL876914 MUS muscu BU24628 G03399852 BB583000 BB583000 CC220090 WS0108.BZ AG542847 RPCI-11-3

us-10-039-183a-14.rst

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OM nucleic

Run on:

Sequence:

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AU175828 529 bp mRNA linear EST 11-JUN-2003
AU175828 Marsupenaeus japonicus adult Marsupenaeus japonicus CDNA
clone PJA553 reverse, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                          Marsupenaeus japonicus
Marsupenaeus japonicus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                           Penaeidee, Mareupenaeus.

(bases 1 to 529)

Rojtinnakorn, J., Hirono, I., Itami, T., Takahashi, Y. and Aoki, T.
Rojtinnakorn, J., Hirono, I., Itami, T., Takahashi, Y. and Aoki, T.
Gene expression in haemocytes of kuruma prawn, Penaeus japonicus, in response to infection with WSSV by EST approach
Fish Shellfish Immunol. 13 (1), 69-83 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="hemocytes"
/dev_stage="adult"
/clone_lib="Marsupenaeus japonicus adult"
/note="Vector: lambda ZAP II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konan 4-5-7, Tokyo, Minato-ku 108-8477, Japan
Tel: 81-3-5463-0689
Fax: 81-3-5463-0690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Marsupenaeus japonicus"
|mol_type="mRNA"
|db_xref="taxon:27405"
|clone="pJAS53"
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Pred. No. 7.9e+02;
); Mismatches 3;
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TBR548667
CL1032403
CL108109
CL168109
BM25780
BM2370495
AW897235
AW8972319
AW897234
BP021697
CCL876916
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AG539002
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Location/Qualifiers
1. .529
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Contact: Takashi Aoki
Aquatic Biosciences
Tokyo University of Eisheries
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CE26558 1008465 H
AG124859 Pan trog1
BX165051 Danio rer
CD701672 EST18196
B1493718 df104902.
B1493719 df104902.
BP57156 BP507156
BP57156 BP507156
BP57156 PUDAP/4TD
CC69387 OCWBN46TV
CC69387 OCWBN46TV
CC69389 PUPIWIZ7TB
CC67577 OCUME74TV
CC67577 PUHUU32TB
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CC673195 PUHUU32TB
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AL746669 Danio rer
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                                                                             April 24, 2005, 00:31:54 ; Search time 1536.18 Seconds (without alignments) 718.576 Million cell updates/sec
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Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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Louses, I. To sooi, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submitssion

Direct Submitsed (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehilro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library FTB This BAC end was generated during the R&D process and may have higher chance of elone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG124859 678 bp DNA linear GSS 04-NOV-2001
Pan troglodytes DNA, clone: PTB-134P02.F, genomic survey sequence.
AG124859
                                                                                                                                                                                                                                                           /tissue type="Adipose"
/clone lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplEx"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
Unpublished
(bases 1 to 678)
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 1.3e+03;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-134P02.F"
/sex="male"
                                                               FORWARD: CTCGGGAAGCGCGCATTGTGTTGGT
BACKWARD: AATAGACTCACATAGGGCGAATTG
Seq primer: GTTGGTACCGGGAATTC.
Location/Qualifiers
                  Email: dgong@medicine.umaryland.edu
PCR PRimers
                                                                                                                                                     1. .466
| Organism="Homo sapiens"
| Mol_type="mRNA"
| db xref="taxon:9606"
| SeX="Male and Pemale"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation:
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM7869 row: H column: 12
Seq primer: -21M13 forward primer (ABI).
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                                                               CB045088

498 bp mRNA linear EST 17-JAN-2003
NISC gc08d06.x1 NCI_CGAP_Col7 Homo sapiens cDNA clone IMAGE:3217979
33, mRNA sequence.
CB045088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_CO17"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 49 hum. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 466)
Yang,R.-Z.; Shuldiner,A. and Gong,D.-W.
EST analysis of human adipose gene expression
Unpublished (2002)
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1 Similarity 92.3%; Pred. No. 1.1e+03;
24; Conservative 0; Mismatches 2; Indels
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Division of Endocrinology, Diabetes and Nutrition
University of Maryland
Followood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="juvenile granulosa tumor"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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76.6%; Score 22.2; DB 4; Length 534;
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Fax: 617 738 6996
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Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 148G22. 148G22
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
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                                                                                                                                                                BX165051 840 bp DNA linear GSS 28-JAN-2003 Danio rerio genomic clone DKEY-148G22, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 373)
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EST18196 human nasopharynx Homo sapiens CDNA, mRNA sequence.
CD701672
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Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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77.9%; Score 22.6; DB 9;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 0; Mismatches 4;
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Mismatches
                                                         799 GTGGACACACACATTTAAAAAAATAAC 827
                                    1 GTGGAGAACACACAATGAAAAAAATATC 29
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                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
Danio rerio
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Homo sapiens
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Contact: YiXin Zeng
25; Conservative
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CD701672/c
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df104g02.wl Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE2541123 3', mRNA sequence.
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1 (bases 1 to 534)
Robertson, N.G., Khetarpal, U., Gutlerrez-Espeleta, G.A., Bieber, P.R. and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA Glbrary using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAMG399 row. N column: 4 Seq primer: 77 primer. Location/Qualifiers
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/nore="ESTS generated from a normal nasopharynx"
library from southern Chinese"
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                     Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ccmorton@bics.bwh.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                          256 GCAGAACACAAAAGGAAAAAAATATC 230
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EST 16-SEP-2003

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL MEDLINE PUBMED COMMENT

AUTHORS REFERENCE

TITLE

RESULT 8 BI493719/c DEFINITION

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E 1 (bases 1 to 816)
S Hayakawa, S., Hwang, J.S., Nishimiya-Fujisawa, C., Ogura, A., Ikeo, K., Hayakawa, S., Hwang, J.S., Nishimiya-Fujisawa, C., Ogura, A., Ikeo, K., Hujawa, T. and Gojobori, T. Hydra EST project
Unpublished (2003)
Contact: Jung Shan Hwang
Center for Information Biology and DNA Data Bank of Japan
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6848
Fax: 81-55-981-6848
Email: jhwang@lab.nig.ac.jp, URL:http://www.cib.nig.ac.jp.
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Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
        BPS07156
BPS07156 Hydra magnipapillata cDNA library Hydra magnipapillata cDNA library Hydra magnipapillata cDNA clone hm_03095, mRNA sequence.
                                                                                                                                                                     Hydra magnipapillata
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
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Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /...organism="Hydra magnipapillata"
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Pred. No. 1.7e+03;
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88.3%; Pred. No. 1...
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Unpublished (2003)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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BZ722055
BZ722055.1 GI:28515434
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                                                                                                                                                 Hydra magnipapillata
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1 (bases 1 to 582)

Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.

Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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df104g02.yl Morton Fetal Cochlea Homo Bapiens cDNA clone
IMAGE:2541123 5', mRNA Bequence.
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DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Repardments of Pathology
Brigham and Women's Hospital
Brigham and Women's Hospital
T. Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6329 row: N column: 4
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                            Indels
No. 1.76+03;
                   Best Local Similarity 88.9%; Pred. No. 1.7e
Matches 24; Conservative 0; Mismatches
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                                                                                   3 GGAGAACACAATGAAAAAAATATC
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Matches 24; Conserve
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/organism="Zea mays"

RESULT 9 BP507156/c

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Plate: 0345 row: N column: 12
Seq primer: M13r
     GI:28518673
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BACKWARD: M13r
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/clone=l1b="zm_0.6_1.0 KB"
/note="Vector: pcR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGWDN46TH
Contact: Cathy Whitelaw
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/mol type="genomic DNA"
/strain="873"
/db xref="texon:4577"
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/clone="lb="Zw0"
/note="Vector; p865K-; Site 1: HincII; 0.7-1.5 |
methylation filtered genomic DNA library"
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                                                                                                                                                   75.2%; Score 21.8; DB 8; Length 101; 92.0%; Pred. No. 2.4e+03; ive 0; Mismatches 2; Indels
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Seg primer: TF
Class: sheared ends.
Location/Qualifiers
1. 678
                                                                                                                                                   Query Match . 75.2
Best Local Similarity 92.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
Zea mays
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1 (bases 1 to 234)

Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.
Sequencing of the maize genome
Unpublished (2003)

Contact: Rod Wing
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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CoT selected genomic DNA library"
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ZMMBBb0345N12.r ZMMBBb Zea mays genomic clone ZMMBBb0345N12 3',
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0089, USA
Tel: 520 625 3967
Fax: 520 621 9288
                                                                                     1 (bases 1 to 795)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5643 Fax: 301-838-0208 Email: whitelaw@tigr.org
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Best Local Similarity 92.0%; Pred. No. 2.4e+03;
Matches 23; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                     Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
TIGR
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CG909969.1 GI:39609239
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Class: sheared ends.
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Zea mays
Zea mays
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826 bp DNA linear GSS 25-MAR-2003 PUFIM27TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa351E05, genomic survey sequence.
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1 (Dases 1 to 826)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.

Maize Genomics Consortium
Other GSSs: PUFIM27TD
Contact: Cathy Whitelaw
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COT selected genomic DNA library"
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/lobe libe"ZMMBBb"
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/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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 Class: BAC ends
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RESULT 15

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CC697577 831 bp DNA linear GSS 19-JUN-2003
OGUME74TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0473M03,
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                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                              1 (base 1 to 811)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUME74TH
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-818-5843
Fax: 301-818-0208
Email: whitelaw@cigr.org
Seg primer: TF
Class: sheared ends.
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1. .831
                                         genomic survey sequence.
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Sequence

Perfect score:

Sequence:

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Run on:

Scoring table:

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Minimum | Maximum |

Database

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Sequence 14, Application US/08831310
; Sequence 14, Application US/08831310
; Publication No. 1200220226035A1
; GENERAL INFORMATION:
    APPLICANT: Kleanthous, Harold et al.
    TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
; TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Blbing LLP
                                                                                  Sequence 20083, A Sequence 60506, A Sequence 60506, A Sequence 1174, A Sequence 1100, App Sequence 11304, App Sequence 13941, Sequence 13941, Sequence 13941, Sequence 13941, Sequence 2, Applisequence 2, Applisequence 12046, App Sequence 27, Applisequence 27, Appli
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MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:

APPLICATION DATE: US/08/831,310 FILING DATE: 01-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFRENCE/DOCKET NUMBER: 06132/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14:
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Sequence 122, App
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Sequence 481, App
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Sequence 1, Appli
                                                                                                                                                                                            April 24, 2005, 02:04:39 ; Search time 234.451 Seconds (without alignments) 750.949 Million cell updates/sec
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-070-927A-541
US-10-367-094-122
US-10-367-094-122
US-10-367-094-122
US-10-052-482-214
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                                                                                                                                                                                                                                                                                                                                                               gtggagaacacacaatgaaaaaaaatatc 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5633728 seqs, 3035525691 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match
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223.24 222.24 222.25 1.62.25

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Score

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88888

Sequence 1242, Ap Sequence 984, App Sequence 387, App

Sequence 1 Sequence 2 Sequence 2 Sequence

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Sequence 1, Application US/08811310;
Publication No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                 Score 29; DB 9; Length 1000;
Pred. No. 0.99;
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                                                                                                                                                                                                                                                                                                                                        0; Indels
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310
FILING DATE: 01-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                     Query Match
100.0%; Score 29; DE
Best Local Similarity 100.0%; Pred. No. 0.9
Matches 29; Conservative 0; Mismatches
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTGGAGAACACACAATGAAAAAAATATC
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NAME/KEY: Signal Sequence
LOCATION: 106...166
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 176 Federal Street
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ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 1149 base pairs
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Best Local Similarity 100.0
Matches 29; Conservative
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STRANDEDNESS: single
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                                                                              , NAME/KEY: CDS
, LOCATION: (51)
US-09-881-752A-243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-831-310-1
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Sequence 14, Application WS/20030143242A1

GENERAL INFORMATION:
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miler, Charles
APPLICANT: Wiler, Charles
APPLICANT: Wiler
APPLICANT
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                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 29; DB 8; Length 29; Best Local Similarity 100.0%; Pred. No. 0.67; Matches 29; Conservative 0; Mismatches 0; Indels
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Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Helicobacter pylori
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGY: linear
US-08-831-310-14
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US-09-881-752A-243
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LENGTH: 1000
TYPE: DNA
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TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 481:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STRANDEDNESS: double
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Matches 28; Conservative
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                                                                                       APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: Helicobacter GHPO 1360 and GHPO 750
TITLE OF INVENTION: Polypebtides and Corresponding Polynucleotide Molecules
FILE REFERENCE: 06132/037002
CURRENT APPLICATION VUMBER: US/10/039,183A
CURRENT PILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 1149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 29; Conservative 0; Mismatches
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 GTGGAGAGACACACAATGAAAAAAAATATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTGGAGAACACACAATGAAAAAAATATC 29
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                        Sequence 1, Application US/10039183A Publication No. US20030143242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (106)...(1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: sig_peptide
; LOCATION: (106)...(166)
US-10-039-183A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-335-977-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
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APPLICANT: Charles A. Kunsch
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Sateven Barsah
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                       Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE. Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP vectra 486/33
CURRENT APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: CUNROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                    94.5%; Score 27.4; DB 17;
96.6%; Pred. No. 3.3;
tive 0; Mismatches 1;
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...456
SEQUENCE DESCRIPTION: SEQ ID NO: 481:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-070-927A-541/c
; Sequence 541, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309-8512
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OTHER INFORMATION: CBtC
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                                                                                                         Length 4134;
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US-10-367-094-122

i Sequence 122, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
    APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer; FILER REFERENCE: 579452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT PILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 122
LENGTH: 421609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.2%; Score 22.4; DB 18; Length Best Local Similarity 95.8%; Pred. No. 4e+02; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                  3; Indels
                                                                                                  Query Match

80.0%; Score 23.2; DB 9;
Best Local Similarity 89.3%; Pred. No. 1.3e+02;
Matches 25; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                    1851 TGGAGAGCAAACAATGAAAAAATTATC 1824
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Publication No. US20040253710A1

GENERAL INFORMATION:
APPLICANT: ACAMBIS RESEARCH LIMITED
TITLE OF INVENTION: BACTERIAL VACCINE
FILE REFERENCE: N. 84948A

CURRENT APPLICATION NUMBER: US/10/489,242

CURRENT FILING DATE: 2004-03-11

PRIOR APPLICATION NUMBER: GB 0121998.9

PRIOR PILING DATE: 2001-09-11

SOFTWARE: PALENTIN VOS: 41

SOFTWARE: PALENTIN VERBION 3.1
;
SEQUENCE DESCRIPTION: SEQ ID NO: 541:
US-09-070-927A-541
                                                                                                                                                                                          2 TGGAGAACACACAATGAAAAAAAATATC 29
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; LCCATION: (1)...(421669)
; OTHER INFORMATION: n = A,T,C or G
US-10-367-094-122
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LOCATION: (1858)..(3579)
OTHER INFORMATION: cstB
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NAME/KEY: gene
LOCATION: (378)..(1103)
OTHER INFORMATION: GELA
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NAME/KEY: gene
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APPLICANT: MORTIS, DEVIC
APPLICANT: MORTIS, DEVIC
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT PILING DATE: 2002-08-15
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-13-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 241
SEQ ID NO 214
SEQ ID NO 214
LENGTH: 96589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22.2; DB 18;
Pred. No. 2.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.6%; Score 22.2; DB 17; Best Local Similarity 88.9%; Pred. No. 4e+02; Matches 24; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40453 GCAGAACACAAAAGGAAAAAAAATATC 40427
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US-09-795-668-1
Sequence 1, Application US/09795668
; Patent No. US20020045577A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.6%;
Best Local Similarity 88.9%;
Matches 24; Conservative C
                                                                                                                                                                                                                            Olham.
FEATURE:
FEATURE:
NAME/KEY: gene
"""TON: (3580)..(4131)
                                                                                                                                                     FEATURE:
NAME/KEY: gene
LOCATION: (3577)..(3579)
OTHER INFORMATION: CSLF
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LOCATION: (4153)..(4659)
COTHER INFORMATION: CETH
US-10-489-242-7
NAME/KEY: gene
LOCATION: (2668)..(3579)
OTHER INFORMATION: CSLD
                                                                 PEATURE:
NAME/KEY: gene
LOCATION: (3031)..(3579)
OTHER INFORWATION: CSLE
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Ouery Match
74.5%; Score 21.6; DB 9;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 24; Conservative 0; Mismatches 4;
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Sequence 1, Application US/09946807

Sequence 1, Application US/09946807

Sequence 1, Application US/09946807

Setal No. US20020165144A1

APPLICANT: Stefansson, Hreinn

APPLICANT: Stefansson, Hreinn

APPLICANT: Gulcher, Jeffrey R.

TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

FILE REFERENCE: 2345.2004-001

CURRENT PILING DATE: 2001-09-05

PRIOR PILING DATE: 2001-09-05

PRIOR PILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US/09/795,668

PRIOR PILING DATE: 2001-02-28

PRIOR PILING DATE: 2001-02-28
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                                                NUMBER OF SEQ ID NOS: 1531
SOFTWARE PREUSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
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SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1
PRIOR APPLICATION NUMBER: US 09/515,715 PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                CCCATION: (1)...(1531)

OTHER INFORMATION: r=g or a
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: y=L/u or c
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: m=a or c
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: k=g or t/u
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: s=g or c
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: s=g or c
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: w=a or t/u
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: b=g or c t/u
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: b=g or c t/u
NAME/KEY: mise feature
LOCATION: (1)...(1531)

OTHER INFORMATION: d=a or g or t/u
NAME/KEY: mise feature
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INFORMATION: h=a or c or t/u
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OTHER INFORMATION: v=a or g or NAME/KEY: misc_feature
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                                                                                                                                                           TYPE: DNA
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Pred. No. 7.9e+02;
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                                             APPLICANT: Steinthorsdottir, Valgerdur APPLICANT: Gulcher, Jeffrey R.
TITLE OP INVENTION: HUMAN SCHIZOPHRENIA GENE FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
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TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE PILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
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OTHER INFORMATION: b=g or c or t/u
NAME/KEY: miloc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
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LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc feature
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Patent No. US20020094954A1
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INFORMATION: v=a or g or c
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LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc feature
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OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
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Best Local Similarity 85.7%;
Matches 24; Conservative
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APPLICANT: Stefansson, Hreinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or
NAME/KEY: misc_feature
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OTHER INFORMATION: m=a or c
NAME/KEY: misc feature
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OTHER INFORMATION: 8=g or c
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LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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Length 1503841;

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Sequence 20083, Application US/10425114

1 Sequence 20083, Application US/10425114

2 Fublication No. US20040034888A1

3 GENERAL INFORMATION:

4 APPLICANT: Liu, Jingdong

5 APPLICANT: Screen, Xieven B

5 APPLICANT: Screen, Steven B

6 APPLICANT: Cao, Yongwei

7 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

7 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

7 TITLE OF INVENTION: NUMBER: US/10/425,114

7 CURRENT FILING DATE: 2003-04-28

7 WUMBER OF SEQ ID NOS: 73128

7 SEQ ID NO 20083

7 LEMPER OF SEQ ID NOS: 73128

7 LEMPER OF SEQ ID NOS: 73128
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                                                                                                                                                                  Length 523;
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                                                                                                                                                                                                               Indels
                                                                                                                                                             Query Match 73.1%; Score 21.2; DB 17;
Best Local Similarity 88.5%; Pred. No. 5.1e+02;
Matches 23; Conservative 0; Mismatches 3;
                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT3847_87934C.1
US-10-424-599-129489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: LIB3170-088-C1_FLI
US-10-425-114-20083
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                   TYPE: DNA ORGANISM: Glycine max
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LENGTH: 523
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LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
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LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
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LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
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LOCATION: (1)...(1531)
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OTHER INFORMATION: k=g or t/u
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LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
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OTHER INFORMATION: y=t/u or
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OTHER INFORMATION: 8=g or c
FEATURE:
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OTHER INFORMATION: v=a or g
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OTHER INFORMATION: m=a or c
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OTHER INFORMATION: r=g or a
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Best Local Similarity 85.7
Matches 24; Conservative
                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
                        ORGANISM: Homo sapiens
                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
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Sequence 129489, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPL

RESULT 14 US-10-424-599-129489/c

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29; Conservative
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LOCATION: (106)...(1002)
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; NAME/KEY: sig_peptide
; LOCATION: (106)...(166)
US-09-336-115C-23
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Best Local Similarity
Matches 29; Conserv
US-09-336-115C-23
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13001, A
12870, A
12880, A
13088, A
13088, Ap
13189, Ap
15339, A
1348, A
10040, A
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14855, A
12569, A
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17056, A
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16001, A
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13134, A
                                                          April 24, 2005, 00:51:24 ; Search time 56.3662 Seconds (without alignments) 841.853 Million cell updates/sec
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): /cgn2_6/ptodatea/1/ina/PCTUS_COMB.seq:*
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         5.1.6
Compugen Ltd
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S-09-107-532A-3580
S-09-248-796A-10040
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S-09-270-767-13134
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S-09-949-016-14855
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US-09-489-039A-378
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Maximum Match 100%
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Best Local Similarity 88.5'
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Matches 23; Conser
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; ORGANISM: Human
US-09-949-016-14870
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US-09-949-016-12350
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US-09-949-016-12350
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Sequence 13001/c

Sequence 13001, Application US/09949016

Sequence 13001, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLO01307

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13001

LENGTH: 136265
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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Pred. No. 71;
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                PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12756
LENGTH: 136264
                                                                                                                                                                                                                                                                                                                                                                                                              3 GGAGAACACACAATGAAAAAAAATATC 29
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Patent No. 6812339
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LCCATION: (1)...(136264)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12756
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13001
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Best Local Similarity 88.9%;
Matches 24; Conservative
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Matches 24; Conservative
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                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-09-949-016-14870
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 05/99/949,016

CURRENT PELING DATE: 2000-04-14,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: 2000-09-08

NUMBER: PRIOR FILING DATE: 2000-09-08

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 12350
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03
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Pred. No. 1.68+02;
0; Mismatches 3; Indels 0;
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Pred. No. 1.6e+02;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 14870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12350, Application US/09949016; Patent No. 6812339
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; ORGANISM: Human
US-09-949-016-15339
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US-09-107-532A-3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                               Query Match 73.1%; Score 21.2; DB 4; Length 193689; Best Local Similarity 88.5%; Pred. No. 1.6e+02; Matches 23; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Steller, Hermann
APPLICANT: Grether, Megan E.

APPLICANT: Mite, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
NUMBER OP SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Manilton, Brook, Smith & Melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9e+02
                                                                                                                                                                                                                                                                                        104097 GAGAAACACAATGAAATAAATGTC 104122
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13088
LENGTH: 193689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/123,343A
PILING DATE: 17-SEP-1993
CLASSIPICATION: 800
PRIOR APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5907A
                                                                                                                                                                                                                                                4 GAGAACACACAATGAAAAAAATATC 29
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08123343A Patent No. 5593879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3990 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%;
85.2%;
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Best Local Similarity 85.2
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02173
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2504 TGATGAACAACAATGACAAAAATAT 2478

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 FRIOR FILING DATE: 1998-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARR: PATENT NOS: 6812 SOFTWARR: Patentin version 3.1 SEQ ID NO 2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.0%; Score 20.6; DB 4; Best Local Similarity 85.2%; Pred. No. 2e+02; Matches 23; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10663 AGAACATACAATGAAATAAATGTC 10639
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TGGAGAACACACAATGAAAAAAATAT 28
Sequence 2728, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-15339/c
; Sequence 15339, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecalis
US-09-134-000C-2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
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Gaps

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GENERAL INFORMATION:

APPLICANT: Keith Weinstcock et al

APPLICANT: Keith Weinstcock et al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196 132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 28208

SEQ ID NO 10040
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                Query Match 69.0%; Score 20; DB 4; Length 236474; Best Local Similarity 82.1%; Pred. No. 4.2e+02; Matches 23; Conservative 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.6%; Score 19.6; DB 4; Length 501; Best Local Similarity 84.6%; Pred. No. 3.7e+02; Matches 22; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.3%; Score 19.8; DB 4; Length 267; Best Local Similarity 91.3%; Pred. No. 3e+02; Matches 21; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217201 GTGGATAACTTACAATGAAAAGAATTT 217228
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTGGAGAACACACAATGAAAAAAATAT 28
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-248-796A-10040
; Sequence 10040, Application US/09248796A
; Patent No. 6747137
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                                                                                                                                                                                              ; LOCATION: (1)...(236474)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13418
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; ORGANISM: Drosophila melanogaster
US-09-270-767-29035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
Candida albicans
US-09-248-796A-10040
                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (1)...(23647
                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-767-29035
                        SEQ ID NO 13418
LENGTH: 236474
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LENGTH: 501
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Sequence 13418, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craiq et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 66/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity 82.1%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/055,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-6277
INFORMATION FOR SEQ ID NO: 3580:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...876
SEQUENCE DESCRIPTION: SEQ ID NO: 3580:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 GTGGAGGAGAAAATGAAAAAATTAT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                          CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                              NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-532A-3580
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Sequence 3939, Application US/09949016

Sequence 3939, Application US/09949016

Patent No. 6812339

GENERALI INCORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 93939

LENGTH: 601
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US-09-270-767-13134
Sequence 13134, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13134
LENGTH: 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.6%; Score 19.6; DB 4; Length 882; Best Local Similarity 84.6%; Pred. No. 3.9e+02; Matches 22; Conservative 0; Mismatches 4; Indels
552 GACAACATAGAATGAAATAAATATC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGGAGAACACACAATGAAAAAAATA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13134
                                                                                                                                                 US-09-949-016-93939/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TYPE: DNA
1 ORGANISM: Human
US-09-949-016-93939
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1 gtggagaacacacaatgaaaaaaaatatc 29 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues

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Total number of hits satisfying chosen parameters:

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ALIGNMENTS

GHPO 1360; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR; Helicobacter pylori polypeptide GHPO 1360 5' DNA primer. AAV07969 Btandard; DNA; 29 BP. 97US-00831310. 97US-00834666. 98WO-US006421 (revised)
(first entry) Synthetic. Helicobacter pylori. 31-MAR-1998; 01-APR-1997; 01-APR-1997; WO9843479-A1 08-OCT-1998. 25-MAR-2003 02-FEB-1999 primer; 88 AAV07969; RESULT 1

(INWR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.

Algarawi A; Tomb J, Miller C, Kleanthous H, Lissolo L,

WPI; 1998-568251/48.

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.

Claim 5; Page 155; 184pp; English.

This 5' primer is used with a 3' primer (see AAV07970) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07963) encoding the unprocessed form of a 32 kDa polypeptide (see AAW73034) designated GHPO 1360. The isolated

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Matches
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                                                           RESULT 3
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polynucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                     GHPO protein, Helicobacter infection, gastroduodenal disease, gastritis, peptic ulcer disease, ss.
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100.0%; Score 29; DB 2; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 29; Conservative 0; Mismatches 0; Indels (
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                                                              every macon 100.0%; Score 29; DB 2; Length 29; Best Local Similarity 100.0%; Pred. No. 0.57; Matches 29; Conservative 0; Mismatches 0; Indela
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                                              Sequence 29 BP; 16 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                 1 GTGGAGAACACACAATGAAAAAAAAATATC 29
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persiste even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vacches to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PF field.)
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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoseactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immunosent seponse that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 to correct PP field.)
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useful in serological diagnosis and protective vaccines, providing long-
lasting immune response.
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                                                                                                                                                                                                                                                                                                            Claim 27; Page 119; 402pp; English.
                                                                             (GENE-) GENELABS TECHNOLOGIES INC.
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                   25-APR-1997;
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                                                      Antigen, immunogenic cluster family, vaccine, gastritis, diagnosis, peptic ulcer, gastric adenocarcinoma, gastric lymphoma, ss.
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               Nucleotide sequence of clone Y104.1.ASM from cluster 3.
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Pred. No. 0.69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence from clone Y104-1.asm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page 123-124; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Fry KE, Lim MY, Mcatee CP;
                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV90580 standard; DNA; 1117 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                              98WO-US008487.
                                                                                                                                                                                                                                                                                     97US-0045107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US008487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
ses 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-009433/01.
                                                                                                                  Helicobacter pylori.
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                                                                                                                                                              WO9849314-A2
                                                                                                                                                                                                                                              25-APR-1998;
                                                                                                                                                                                                                                                                                       25-APR-1997;
                                                                                                                                                                                                                                                                                                          14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2003
18-FEB-1999
                                                                                                                                                                                                    05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                        Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV90580,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Best Loc Matches

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Inducing immune response to Helicobacter useful for treating Helicobacter pylori infection, by administering immunogenic Helicobacter polypeptide admixed with adjuvant having heat-liable toxin of Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for inducing protective immune response to Helicobacter infection. The method comprising administering to a mammal by injection an immunogenic Helicobacter pylori polypeptide comprising a subunit of H.pylori urease admixed with an adjuvant having one or more heat-liable toxin of Bscherichia coli (LTP), B subunit of LT inducing an immune response to Helicobacter infection in a mammal. The method is useful for both treatment and prevention of H.pylori infection. The invention is useful as vaccine. The present sequence is Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; bacterium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 10; Length 1149; 100.0%; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1149 BP; 412 A; 185 C; 242 G; 310 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 GTGGAGAACACACAATGAAAAAAATATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTGGAGAACACACAATGAAAAAAAATATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .456
/*tag= a
                                                                                                                                                                                                                                                                                                                      Claim 8; Col 105-108; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00625811.
96US-00758731.
96US-00736905.
96US-00738859.
96US-00761318.
99US-00336115
                                          98US-00100258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori ORF 03xe11215orf7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV24638 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pylori p32 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori.
                                                                                    (ACAM-) ACAMBIS INC.
                                                                                                                                                                      WPI; 2003-799824/75.
                                                                                                                              Guy B;
                                                                                                                                                                                            P-PSDB; ABW00787
  18-JUN-1999;
                                          19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9737044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1996;
25-OCT-1996;
28-OCT-1996;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1996;
                                                                                                                              Weltzin RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV24638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA sequence codes for a 32 kDa Helicobacter pylori polypeptide (see AAW73034) designated GHPO 1360. A polynucleotide encoding the unprocessed, or the mature, GHPO 1360 can be obtained from genomic DNA by CR unprocessed, or the mature, GHPO 1360 can be obtained from genomic DNA by CR amplification (see AAW72001, AAW07912-21 and AAW07953-64) encoding a can be compared to 75 kDa Helicobacter polypeptides (see AAW73012-32), GHPO 1360 cand a 50 kDa polypeptide (see AAW73015). These polymucleotides were initially identified in a search of H. pylori genomic databases. DNA cassetters for expression of the Helicobacter proteins (unprocessed or mature forms) in prokaryotic or eukaryotic cells are provided. The polymucleotides can be used in vacciness to prevent or treat Hb infection in a mammal. Viral (especially poxvirus) or bacterial vectors are used. Products and methods of the invention allow treatment and prevention of gastroducdenal diseases associated with Hb infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. Diagnostic and detection methods are also provided. GHPO 1360 was demonstrated to be a protective antigen. (Updated on 25-MAR 2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immune response; Helicobacter infection; adjuvant; heat-liable toxin; LT;
cholera toxin; CT; urease; therapy; antibacterial; vaccine; antigen; p32;
                                                                                                                                           New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 29; DB 2; Length 1149; 100.0%; Pred. No. 0.69; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1149 BP; 412 A; 185 C; 242 G; 310 T; 0 U; 0 Other;
                                            Tomb J, Miller C, Algarawi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAGAACACACAATGAAAAAAATATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTGGAGAACACACAATGAAAAAAATATC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
167. .1002
/*tag= c
/product= "Mature p32"
                                                                                                                                                                                                                                      Claim 1; Page 148-149; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori p32 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD61576 standard; DNA; 1149 BP
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product=
                                            Kleanthous H, Lissolo L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106. .1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106. .166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
                                                                                    WPI; 1998-568251/48.
P-PSDB; AAW73034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6576244-B1
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Best Loca Matches

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AAXI2938 to AAXI391 represent these nucleotide sequences which are primary nucleotide sequences; also known as contigs. The computer-based system can identify fragments of the Enterococcus facetals genome with commercial importance. The products can be used to detect the presence of Enterococcus facetals in samples. They can also be used for diagnosing Enterococcus facetals in samples. They can also be used for diagnosing Enterococcus facetals in samples which can be used to modulate the disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facetals or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus facetals nucleotide sequences can be used in vaccines to
                                                                                New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer readable medium having recorded on it a Enterococcus faecalis nucleotide sequence useful for detecting diseases related to Enterococcus infections in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer readable medium; Enterococcus faecalis; microbe; growth; pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermenting; sugar source; metabolite; vaccine; bioccite technology; antibacterial; modulator of nucleic acid expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4134 BP; 1370 A; 863 C; 578 G; 1315 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                         computer readable medium has been developed which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevent or attenuate an Enterococcal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 23.2; DB
; Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis contig sequence #541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1851 recaecaacaarcaarcaaaaaarrarc 1824
                                                                                                                                                                                                 Claim 1; Page 1795-1797; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TGGAGAACACACAATGAAAAAAATATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABS99273 standard; DNA; 4134 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.3°
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunsch CA, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-750065/81.
                          WPI; 1999-045171/04
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(DILL/) DILLON P J.
(BARA/) BARASH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002120116-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a Helicobacter pylori protein of unspecified function. The protein may be used in a vaccine to prevent or treat H.

The protein may be used in a vaccine to prevent or treat H.

The pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H.

The DNA and probes derived from it may be used for the identification of H.

The DNA and probes complementary to the DNA act as antisense sequences, and can be used to prevent the translation of H. pylori mkNA. Antibodies and distribution of H. pylori—specific antigens. The genemic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed to for one for a least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF mathematical and all and the predicted from various ore processed to the processed of the processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis, contig, detection, Enterococcal infection, vaccine, attenuation, computer readable medium, ds.
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis genome contig SEQ ID NO:541,
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                                                                                                                                                                                                                                                                                                               Claim 5,6; Page 155; 1145pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX13478/c
ID AAX13478 standard; DNA; 4134 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMA-) HUMAN GENOME SCI INC
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                                                                                                           WPI; 1997-503122/46.
P-PSDB; AAW55229.
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(ASTR ) ASTRA AB.
                                                        Alm RA;
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14-NOV-1997;
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                                                        Smith D,
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New bacterial cell expressing three or more coli surface antigens, useful for manufacturing a medicament, i.e. a vaccine, for vaccination against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 76.6%; Score 22.2; DB 10; Length 4746; Local Similarity 88.9%; Pred. No. 1.8e+02; les 24; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4746 BP; 1588 A; 745 C; 957 G; 1456 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ZFHX1B carcinoma associated gene, SEQ ID NO:1226.
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. "cstD gene"
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= "cstF gene"
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note= "cstG gene"
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                                                                                                                                                                     .4659
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/note= '
3580. .
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                               misc_feature
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Continuation (4 of 5) of ABD32627 from base 300001 (Mouse cancer-associated genomic DNA WP Sequence split into 5 fragments LOCUS ABD32627 Accession Abd32627

WP ABD32627_0 100001 110000

WP ABD32627_1 100001 210000

WP ABD32627_3 300001 310000

WP ABD32627_3 300001 410000
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              The present invention relates to a new computer readable medium with an Enterococcus faecalis nucleotide sequence. The invention is useful to diagnose the presence of E.faecalis in a sample or determining the presence of a specific microbe in a sample or determining the confer modulating the growth or pathogenicity of E.faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular sugar source or to produce a particular metabolite. The invention is useful for detecting diseases related to Enterococcus infections in animals, and for detecting E.faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis contig DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coli surface antigen; CS; vaccine; diarrhoea; bacterial infection; antigen; cstB; cstA; cstC; cstD; cstE; cstF; cstG; cstH; gene; ds.
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                                                                                                                                                                                                                                                                              Query Match 80.0%; Score 23.2; DB 6; Length 4134; Best Local Similarity 89.3%; Pred. No. 81; Matches 25; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                   Sequence 4134 BP; 1370 A; 863 C; 578 G; 1315 T; 0 U; 8 Other;
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/*tag= a

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/note= "cstB gene"

2266. .3579
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/note= "cstC gene"
2668. .3579
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ABD32627 0
ABD32627 1
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AAD55747
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Darsley MJ;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant carcinoma associated proteins (ADAD1482-ADAD3034), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (specially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, proseate cancer, integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, proseate cancer, integration into host leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodise are also useful as therement agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at
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                                                                                                                                                                                                         The invention relates to recombinant carcinoma associated (CA) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 96589 BP; 29004 A; 18509 C; 19494 G; 29562 T; 0 U; 20 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                      New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences,
                                                                                                                                                                              Claim 1; SEQ ID NO 1226; 245pp; English.
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                            26-DEC-2001; 2001US-00035832
                                                      (SAGR-) SAGRES DISCOVERY
                                                                                                            WPI; 2003-587068/55.
                                                                                 Morrie DW;
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for screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy; lymphoma; breast cancer; prostate cancer; leukaemia; ds; human, 2PHXIB.
                                                                                                                                                                                                                                                                                                                     recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 96589 BP; 29004 A; 18509 C; 19494 G; 29562 T; 0 U; 20 Other;
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Pred. No. 2.1e+02;
0; Mismatches 3
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30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
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                                                                                                     (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                           Engelhard EK;
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Matches 24; Conservative
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proteins are useful for diagnosing and treating carcinomas, for example lymphoma, breast cancer, prostate cancer or leukaemia, or for screening drug candidates or bioactive agents capable of binding to, or modulating the activity of, a carcinoma associated protein. The present sequence is the genomic DNA sequence of the human ZFHXIB gene which is a carcinoma associated gene of the invention. 888888888

Sequence 96589 BP; 29004 A; 18508 C; 19495 G; 29562 T; 0 U; 20 Other;

ö Gaps Query Match 76.6%; Score 22.2; DB 10; Length 96589; Best Local Similarity 88.9%; Pred. No. 2.18+02; Matches 24; Conservative 0; Mismatches 3; Indels 0;

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Search completed: April 24, 2005, 02:20:02 Job time: 194.542 secs

Sequence Homo Bapi Oryza Bat Homo Bapi

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Perfect score:

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Searched:

Database

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AC116953 Mus muscu
AC098034 Rattus no
CQ572261 Sequence
CQ575118 Sequence
AY061475 Drosophil
CQ575117 Sequence
AC017241 Drosophil
AC084471 Caenorhab
BX890635 Zebrafish
AC067978 Homo sapi
Continuation (2 of
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BX001056 Zebrafish
AC104000 Homo sapi
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A01N43/04,A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
A61K39/40,
G01N33/554,G01N33/569
Strandedness: Single;
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Patent: JP 20015239544 59 27-NOV-2001;
MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERBUMS E:
WACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA, PHUAN GENOME SCIENCES INC
PN JP 2001523954-A/59
PD 27-NOV-2001
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HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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         AX741417 S
AC137616 O
AX695599 S
AY029472 F
AC137621 C
AC00951 C
AC096104 F
AC16106104 F
AC148367
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/db_xref="taxon:10509"

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JP 2001523954-A/59.
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Best Local Similarity 100.
Matches 29; Conservative
                    76.6 94252
76.6 196589
76.6 126332
76.6 129391
76.6 230345
76.6 230345
75.2 184455
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AC01339 Homo sapi
AL122002 Human DNA
CQB70465 Sequence
AL354988 Homo sapi
CQ869727 Sequence
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                     4708233 segs, 24227607955 residues
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Listing first 45 summaries
                                                       nucleic search, using sw model
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Gapop 10.0', Gapext 1.0
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HD061969 1082 bp DNA linear PAT 27-AUG-2002
Antigenic composition and method of detection for Helicobacter
Pylori.
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Antigenic composition and method of detection for Helicobacter
Pylori.
BD061705
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1 (bases 1 to 1082)

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Antigenic composition and method of detection for Helicobacter
Antigenic composition and method of detection for Helicobacter

Antigenic composition and method of detection for Helicobacter

GENELABS TECHNOLOGIES INC

GENELABS TECHNOLOGIES INC

PP 25-APR-1999 UP 60/045107,14-OCT-1997 US

PR 25-APR-1999 US 60/045107,14-OCT-1997 US

C12N15/31,C07K14/205,C07K16/12,A61K39/106

CC Strandedness: Single;

CC Topology: Linear;

FH Key
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C12N15/31,C07K14/205,C07K16/12,A61K39/106
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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    .1082
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JP 2001517091-A/39.
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other sequences; artificial sequences.
1 (bases 1 to 1117)
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100.0%; Pred. No. 2;
:ive 0; Mismatches
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JP 2001517091-A/303.
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AUTHORS
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BD061705
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BD061969
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PN JP 200157393-A/122
PD 25-DEC-2001
PP 01-APR-1999 US 08/881227 PR 29-UUL-1997 US 08/881227 PR 29-UUL-1997 US 08/833457,24-JUN-1997 US 08/881227 PR 29-UUL-1997 US 08/905615
PI HAROLD KLEANTHOUS,AMAL AL GARAWI, CHARLES MILLER, JEAN FRANCOIS PI TOMB,
PI RAYMOND PETER COMEN
PC A01N43/04,A61K31/70
CC Strandedness: Single;
CC Topology: Linear;
FH Key
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construct
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consories artificial sequences.

E 1 (bases 1 to 1082)
Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.
Antigenic composition and method of detection for Helicobacter
Construction of method of detection for Helicobacter
Antigenic composition and method of detection
CENTLASS TECHNOLOGIES INC
PN JP 2001517091-A/50
PD 02-OCT-2001
PP 25-ARR-1998 JP 1998547263
PR 25-ARR-1997 US 60/045107, 14-OCT-1997 US 60/061958 PI
THERESA P CHOW, KIRK B FRY, MOON Y LIM, C P MCATEB PC
                                                                                                                                                                                                                                                                         synthetic construct
synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 1000)
1 (baraui, A.A., Miller, C., Tomb, J.F. and Oomen, R.P.
Identification of polyvuclectides encoding novel helicobacter
polypeptides in the helicobacter genome
polypeptides in the helicobacter genome
MERIEUX ORAVAX SOCIETE EN NOW COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCINS AGROBIOLOGICAL RESOURCES MINISTRY O SA, HUMAN GENOME
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Antigenic composition and method of detection for Helicobacter
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Identification of polynucleotides encoding novel helicobacter
polypeptides in the helicobacter genome.
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Pred. No. 2;
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                             1 GTGGAGAACACACAATGAAAAAAATATC 29
          GTGGAGAACACACAATGAAAAAAATATC 29
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BD061716.1 GI:22607321
JP 2001517091-A/50.
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100.0%;
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Best Local Similarity 100.
Matches 29; Conservative
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G01N33/554, G01N33/569
Strandedness: Single;
                                                              HUMAN GENOME SCIENCES INC
PN JP 2001523954-A/53
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Helicobacter pylori J99
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AE001454.1 GI:4154666
                                                                                                                                                                                                                               Topology: Linear;
Key
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Best Local Similarity 100.0
                                                                                             27-NOV-2001
                                                                            PN JP 27-
PD 27-
PD 27-
PI HAR,
MILLER,
PI AMAR,
PC A01
PC A01
PC A61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT 17-AUG-2003
Chow, T.P., Fry, K.E., Lim, M.Y. and Mcatee, C.P.
Antigenic composition and method of detection for Helicobacter
Patent: 92 201517091-A 39 02-OCT-2001;
GENELABS TECHNOLGGIES INC
PN JP 2001517091-A/39
PD 02-OCT-2001
PP 25-APR-1998 JP 1998547263
PR 25-APR-1997 US 60/045107, 14-OCT-1997 US 60/061958 PI
THERESA P CHOW, KIRK E PRY, MOON Y LIM, C P MCATEE PC
C12N15/31, C07K14/205, C07K16/12, A61K39/106
CC Strandedness: Single;
CC Topology: Linear;
FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
1 (bases 1 to 1149)
Weltzin,R.A. and Guy,B.
LT and CT in parenteral immunization methods against helicobacter
                                                                                                          60/061958 PI
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
1 (bases 1 to 1149)
Kleanthous, H., Lissolo, L., Tomb, J.F., Miller, C. and Garawi, A.A.
76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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100.0%; Pred. No. ...
0; Mismatches
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     169 GTGGAGAACACACAATGAAAAAAATATC 197
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Pred. No.
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                                                                                                                                                                                                 Location/Qualifiers
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100.0%; Pre
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JP 2001523954-A/53.
Mastadenovirus
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Matches 29; Conservative
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Best Local Similarity 100.
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King, B.L., Alm, R.A. and Trust, T.J.

King, B.L., Alm, R.A. and Trust, T.J.

King, B.L., Alm, R.A. and Trust, T.J.

Lorect Subnission

Street, Cambridge, MA 02139, USA

Address all correspondence to: hp@arcb.us.astra.com or Richard

A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge,

MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith,

Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills,

Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics

Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and

Diane E. Taylor are with the University of Alberta Department of

Medical Microbiology and Immunology, Edmonton, Alberta, Canada, TGG

217 and the Canadian Bacterial Diseases Network. All other authors

are with Astra Research Center Boston, 128 Sidney Street,

Cambridge, MA, 02139. Putative identifications, sequence

alignments, and name and sequence search capabiblity are available
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Helicobacter pylori, strain J99 section 15 of 132 of the complete
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Nature 397 (6715), 176-180 (1999)
                                                                                                                                                                                                                                                                                                      Ы
corresponding polynucleotide molecules betant: 19 200123954-A 53 27-NOV-2001, MERLEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
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AOIN43/04,AOIN59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
A61K39/40,
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I (bases I to 10085)
Alm.R.A., Ling.L.S., Moir.D.T., King.B.L., Brown.E.D., Doig.P.C.,
Smith.D.R., Noonan,B., Guild,B.C., deJonge,B.L., Carmel,G.,
Tummino,P.J., Caruso,A., Uria-Nickelsen,M., Mills,D.M., Ives,C.,
Gibson,R., Merberg,D., Mills,S.D., Jiang,Q., Taylor,D.E.,
Vovis,G.F. and Trust,T.
                                                                                                                                                                                                                                                                                                   HAROLD KLEANTHOUS, LING LISSOLO, JEAN FRANCOIS TOMB, CHARLES
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100.0%; Pred. No. 2;
ive 0; Mismatches

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complement (4221. .5393)
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KSEILDYQDGEEGIKGVAFIIKGENDAYGYLKNENGVHRLVRISFAS
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at ARCB's World Wide Web site. (URL:
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Location/Qualifiers
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FFRASLFVIKDIQKGEALTENNIKALRPNLGLHPKFYKEILGQKASKFLKANTPLSAD
DIERSL"
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34.30; identified by sequence similarity; putative"
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complement (3179. .4201)
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                                                         246. .1145
                                                         gene
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Halicobacter pylori 26695
Bacteria; Proteobacteria; Epailonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori 26695 section 16 of 134 of the complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Klark, H.P., Gill, S., Beleischmann, R.D., Ketchun, K.A., Klark, H.P., Gill, S., Dougherty, B.A., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, E.F., Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Bergy, D.E., Gooayne, J.D., Uterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Bowman, C., Watthey, L., Wallin, E., Hayes, W.S., Borodovsky, M., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the gastric pathogen Helicobacter
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Submitted (17-MAR-1999) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location Qualifiers
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                                                                                                                                                                                                               note="similar to H. pylori 26695 gene HP0176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 10085;
                                                                                                                                                                                                                                     'codon start=1
'trans1 table=11
'product="FRUCTOSE-BISPHOSPHATE ALDOLASE"
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/organism="Helicobacter pylori 26695"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                             /note="Bynonym: jhp0162"
8274. .9197
/gene="fba"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 388 (6642), 539-547 (1997)
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                                                                               3274. .9197
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***ches 29; Conservative
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/note="similar to GB:J01620 SP:P00477 GB:V00283 PID:146218 PID:41603 percent identity: 53.96; identified by sequence similarity; putative"
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Enterococcus faecalis V583, section 10 of 11 of the complete
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Enterococcus faecialis polynuclectides and polypeptides

Enterococcus faecialis polynuclectides and polypeptides

Enterococcus faecialis polynuclectides and polypeptides

HUMAN GENOME SCIENCES INC

OS Unidentified

PN JP 2002529046-A/541

PN JP 2002529046-A/541

PP 03-SEP-2002;

PF 04-MAY-1998 JP 1998548302

PR 06-MAY-1997 US 60/06009

PR 06-MAY-1997 US 60/06009

PR 06-MAY-1997 US 60/06009

PR CAPALES A KUNSCH, PATRICK J DILLON, STEVEN C BARASH PC

C12N15/31, C07K14/315, C07K16/12, C12Q1/68

CC Strandedness: Double;

CC Topology: Linear;

CC Topology: Linear;

CC Enterococcus faecialis polynuclectides and polypeptides

Key Location/Qualifiers

FT Source

//organism='Unidentified'.
                                                                                                                                                 /transl_table=11
/product="serine hydroxymethyltransferase (glyA)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bD193947 4134 bp DNA linear PAT
Enterococcus faecialis polynucleotides and polypeptides.
BD193947
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89.3%; Pred. No. 2.2e+02;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                        0; Mismatches
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Pred. No.

    .4134
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/mol_type="genomic DNA"
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                       gene="HP0183"
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JP 2002529046-A/541.
                                                                                                                         /codon_start=1
/transl_table=
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AE016956.1 GI:293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="apolipoprotein N-acyltransferase (cute)"
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/protein_id="AAD07250.1"
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FLSTKPLKKYRIGVLLLGALDFWGFRYDLKYGVIELUSTRTPQDLKFDSSYLND
IENNILKEIKLAQSKGKTL VPPETAYPIALENSPFRAKLEDLSDNIAILIGTLRTPG
YNLYNSSFLFSKESVQLADKVILLAPFGETAYPIALENSPFRAKLEDLSDNIAILIGTLRTPG
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                                                                                                                                                                                                                                                 /translation="MIKAINISHAFEKPLYNGVNLHIKPKESLAILGVSGSGKSTLLS
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NLDTYSANQVISMLQYXITEKGGALVLATHDEHLAFTCSQVYRLEKEVLIKEK"
complement (4843. .6120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MVVVAFGIRGFYHGFVSEVAGTLGIVLGVYLASRYSVAVGNLFS
EHLYDLKNEFWYNLIGPLIVLASIWVFFLAFGYLLGKYLLYFSGLGIIDKALGFFFSCL
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KTELVLSFILYALSKMFWKDANAYLOGEKAPFSTWKSVASKIMRLDGVKHVEGNLKD
NLEBNSDEVKRKESFNKKJESFNKAMRGYGFELKEKAROLPKRMLDPRANQTPPNPTP
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LEVERYLRIAPELYLKRLIVGGFEAVFEINRNFRNEGMDHSHNPEFTMIEFYWAYHTY
EDLIELSKRLFPYLLKTLINLDSKIIYNDMEVDFNOGTSVIZYLDALETTGGISKOILEK
EDRILAYLLEGGIKVEPNLYGKLLABPOPPVEHQLINPTFYTQYPIEISPLARRND
SNPNIADRYFELFIAGKEIANGFSELNDPLOGLERFKNOYABEKEKGBEBAQYMBEDYW
ALAHGMPPTAGGGIGIDRLVMLLTGAKSIKDVILFPAMRPVKNDFNVESEE"
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VKGLEEPKDKEKCESIVGRVKLLRLMGKACFIKVEDESTILQVYVSQNELNDEFKSLK
KHLEVGDIVLVKGFPFATKTGELSIHALEFHILSKTIVPLPEKFHGLSDIELRYRQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:M63448 SP:P41258 PID:144208 percent identity: 58.63; identified by sequence similarity;
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/note="similar to GP:1786703 percent identity: 37.62;
identified by sequence similarity; putative"
/codon start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by GeneMark; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:L42023 SP:P44626 PID:1003497 PID:1222229 PID:1204555 percent identity: 28.03; identified by sequence similarity; putative"
                                                                                                                                                                         ATP-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
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/db_xref="GI:2313270"
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                                                                                                                                                 /transT_table=11
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/protein_id="AAD07249.1"
/db_xref="G1:2313268"
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/protein_id="AAD07253.1"
/db_xref="GI:2313272"
                          complement (4205. .4846)
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6378. .7052
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/gene="HP0182"
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/gene="HP0182"
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gene

CDS

REFERENCE AUTHORS JOURNAL

TITLE

AUTHORS PUBMED REFERENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="aminoglycoside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6496)
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complement(6664. .7527)
                                                                                                                                                                                                                                                SVEDLSIFIDSMAAEVHNYSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (6664. .7527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="EF2861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="EF2862"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSLRLKDLQGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649. .8230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7649. .8230
                                                                                                                                                                                                                                                                                                                                                                                                                               PF01361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF03734"
                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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EKGNIEGKDILDIAMKAVEKVIPEEIAFDDRTLQAVIIFKRMNAASOMIVFIKNEGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGEIATIGEHTAEISGVSTGTDWTRDYSQSGALRSLLGTVSTEKQĞLPAEEVDEYLKK
SYARNDRYGYGPTİKQEKĞILENGYEDYLQKKKASBYULNINGKTYĞQTPİKGKEĞSILLİLTID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTMOLTAEQALEYSSNAYMKLVFKMYGVNYYPNMIFPYEVBODTVFKELRKAFAEYG
MGTKYGLDI DEBETTGIQNKPKOSSSAPOGGGNLLDLSFGGYDTYSALQLAQYYSYAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSIHITFPDGAVKPFDSGITTFDVAKSISNSLAKKALAGKFNGV
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FYYDTDNGESPVTAEDLPAIEAEMMKIVKENNPIVRKEISRAEALELFADDPYKVELI
                                                                                 Lateran L. Banerjei, L., Myers, G.S. A., Nelson, K.E., Seshadri, R., Paulsen, I., Banerjei, L., Myers, G.S. A., Gill, S.R., Heidelberg, J.F., Tectellin, H., Dodson, R.J., Umayam, L., Brinkac, L., Beanan, M., Daugherty, S., DeBoy, R.T., Durkin, S., Kolonay, J., Madupu, R., Kolonay, J., Wanthevan, J., Tran, B., Upton, J., Hansen, T., Shetty, J., Khouri, H., Utterback, T., Radune, D., Ketchum, K.A., Dougherty, B.A. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pauleen, I., Banerjei, L., Myers, G.S.A., Nelson, K.E., Seshadri, R., Read, T.D., Fouts, D.B., Elsen, J.A., Gill, S.R., Heidelberg, J.F., Uretteiln, H., Dodson, R.J., Umayam, L., Brinkac, L., Beanan, M., Daugherty, S., DeBoy, R.T., Durkin, S., Kolonay, J., Mauthevan, J., Tran, B., Upton, J., Hansen, T., Shetty, J., Khouri, H., Utterback, T., Radune, D., Ketchum, K.A., Dougherty, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-FBB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus_tag="EF2858"
note="identified by match to PFAM protein family HMM
                                                                                                                                                                                                                                                                                                                              Role of Mobile DNA in the Evolution of Vancomycin-Resistant
Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (94. .2229)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Enterococcus faecalis V583"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="threonyl-tRNA synthetase"
protein id="AAO82550.1"
db xref="G1:29344793"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPHLNDEASKPNOTIAKEVLEAYMEMYKK"
complement (2394. .4331)
                                                                                                                                                                                                                                                                                                                                                                                          Science 299 (5615), 2071-2074 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="taxon:226185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2394. .4331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus_tag="EF2858"
   Enterococcus faecalis V583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'codon_start=1
'transI_table=
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transI table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 304454)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="thrs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .304454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                      12663927
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ORGANISM
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IERYIVDKEISLGYQHVYTPIMADVELYKTSCHWDHYHEDMFPPMDMCDGEMLULRPM NCPHHWMYKNDIHSYRELPIRIAELGWMHYYEKSGALSGLQRVREWTLNDGHTFVRP DOKKDEFKRTLELMVAYYADFNITDYRRFLSYRDPMYDKYFDDDAMWEKAQANLKAA MDELELDYFREAGGEARYGRLYOYYKTALGMEETLSTIQLDFLLFBRFDLYVGEDG ENTHREVVIHRGIYSYMRRFYAYLTEYYKGAFFTWLAFIQATIIPSYTGYGEG KRRLQAQCIRVEVDDRNEKMGYKIRASQTQKVPYQLVVGDKEMEDATVNVRRYGSKET /product="4-oxalocrotonate tautomerase, putative" |protein id="AA082251.1" |db_xref="G1:234194" |translation="MPFVHVELIEGRTEEQLTNMVKDITEAVSKNAGAPKENIHVIVN KVNGVSVGWINVNAAEEKIAÕVNQTEEVVVQTGTKEEKIQLPKKYQLDQKFLKDHLHS SKVKLPLNERFKKELEAKLATLSPPGKPSKNASIRRGNGTFEIVPEEQGTVVDTQRL NQQIIADVPAGGKGNYQYNAKPSYKAPEITKEDQTLKATLTLNKLNKTITVDINGEK VAFDKTQIQNVLNDDGTINKELLTYTVQLETTYGSANQPVLFTDVHGTTRRFKRNGS YGWSIDGAKTQELLYNALNSQEQTNATAPLVGDTKENSKIANNYIEIDLKDQXMYG IDGKKIVTTDVITGRYNKGTATVPGFHTILYRTTDVNLEGGMLDGSRYSVPKYMPL /trānslation="MRTEBEMFQLIMDVAKQEBHIRAVGMVGSRTNVKAPKDSPOPPD ITVIVBPCABFFBTATWIAKFGQPLIMQRPKGMTLFPTEPKTRETFLMLFBDGRIDL TLOYIVBPCABFTATWIAKFGQPLIMQRPKDFDVASDKAYTVTVPDQQQPNDCCNBFWW VSTYVVKGLCRNBETSAVTHLYBYZCQOBLLBLLSMQAMQBEPEPISVGRFKTKNYV TPDTMDQLASLLDFSSKEACWNSLIKTQAFFDVVAQDFAKMQFPFYTHLQBAKKVTEYT /product="conserved hypothetical protein"
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complement(4728. .4907)
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation and not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TREMBL; Swi, SWISSPROT; Tr:, TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
VECTOR: pBAC63.6
IMPORTATY: This sequence is not the entire insert of clone
RP11-147111 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-147111 is at 110098 in this
sequence. The true right end of clone RP11-143M1S is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-147111 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                 requests: clonerequest@sanger.ac.uk on or before May 15, 201 this sequence version replaced gi:7798790, gi:1296443: During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="LiMC4 repeat: matches 7681, .7936 of consensus"
2201. .5316
/note="LiMC5 repeat: matches 7326. .7442 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 7066. .7165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MLT11 repeat: matches 327. .399 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 23. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSx repeat: matches 2. .311 of consensus"
E-mail enquiries: humquery@Banger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSq repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2261. .2319
/note="MIR repeat: matches 146. .204 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064. 3386
Thote="AluJb repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MER53 repeat: matches 1. .118 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      consensus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7204 of
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/note="AluJb repeat: matches 1. .302 of
4795. .5042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-147111"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1MC5 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note="L1MC5 r
6813. .7013
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                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MIAFFVVIAVL&ITACREPKEKKVTASTEASSKVEETNEKTSET IDKTNEQASSSVESNESVKNEEPTADGNNSQLTVADLDTTAINAGDFTTLVGIMKNGK GESLIIHPDGSTNTGANITKDSPTDERPITSLSIRMGPTGAALLIVKIGVENPNGDO SDKTKPRLLITQDSGNYFRSSEERONGOGNEEAKIIDTQEKAETYIRKTLTDA ENNDTNIGFLGANNGPFFRAQSKQMAANGGTGTVGFFRVSPQGAVRITDARGN" complement (10676. 11395)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Human DNA sequence from clone RP11-147111 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and SP:031509; identified
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110098)
                                                                                                                                                /locus tag="EF2863"
/note="similar to GB:X59372, GB:X15506, SP:P17482,
SP:P28356, PID:32391, PID:32398, GB:X59372, GB:X15506,
SP:P17482, SP:E28356, PID:32391, and PID:32398,
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/protein_id="AAO82557.1"
/db_xref="GI:29344800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 23.2; DB 1; Length 304454; 89.3%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                             product="endo-beta-N-acetylglucosaminidase"
protein id="AAO82555.1"
db_xref="GI:29344798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
NVSGITAASSFPKDIKNFGRELLSLGYALLFDW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (10676, 11395)
| Journ Lag="EF2866" | Journ Lags" | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall | Journ Lo Gall |
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                                         8388. .9332
/locus_tag="EF2863"
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AL358976.11 GI:13273751
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Conservative
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Direct Submission
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Matches 25; Conserv
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Homo sapiens
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AL358976/c
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JOURNAL
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KEYWORDS
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12836. .13671

// Note="LiME3A repeat: matches 5237. .6095 of consensus"

13734. .14362

// Note="LiM4 repeat: matches 4342. .5025 of consensus"

14363. .14660
                        253. .8047
note="LlWA4A repeat: matches 5507. .6299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches 5347. .5680 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LiME1 repeat: matches 5887. .6042 of consensus"
1132. .21426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Alusx repeat: matches 1. .295 of consensus" 11427. .22078 note="Limel repeat: matches 5200. .5887 of consensus" 3672. .23963
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29949. .30243
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note="LIP3 repeat: matches 5606. .5747 of consensus"
15396. .25559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1M4 repeat: matches 4911. .5495 of consensus"
                                                                                                                                                                                                                                    9589. 9874
/note="AluJo repeat: matches 1. .281 of consensus"
9883. 9940
9883. 9940
10342. "10652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote="12 repeat: matches 2297. .2600 of consensus" 1926. .19508
Anote="AluJb repeat: matches 1. .288 of consensus" 1918. .19826
Anote="12 repeat: matches 2480. .2714 of consensus" 20588. .20764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6436. .16546
note="L2 repeat: matches 1795. .1884 of consensus"
.7490. .17651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2600. .2749 of consensus" 7652. .17905
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/note="MER5A repeat: matches 13. .115 of consensus"
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4857. .24884
4857. .24884
4867. .25173
4886. .25173
foote="AluJb repeat: matches 1. .285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 77. .241 of consensus"
16182. .26479
'note="AluSx repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MERSA repeat: matches 2. .189 of consensus" 29450. .29803
                                                                                                                                                                       0041. 9145
note="MERSB repeat: matches 1. .110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSx repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .253 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSx repeat: matches 1. .296 of consensus"
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note="MIR repeat: matches 3. .232 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                        1405. 11454
note="25 copies 2 mer aa 78% conserved"
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note="AluSg repeat: matches 1.
7906. 18099
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Zebrafish DNA sequence from clone DNA linear VRT 16-MAR-2004 Zebrafish DNA sequence from clone DKEY-171P23 in linkage group 5, BX088597 ...
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Submitted (13-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, Calol ISA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 13, 2004 this sequence version replaced gi:45379346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                     .2454 of consensus"
                                                                                                                                                                         fnote="11u3b repeat: matches 1. .306 of consensus" 15496. .35679
Thote="MIR repeat: matches 11. .197 of consensus" 15731. .35765
Inote="U2 repeat: matches 1. .35 of consensus" 15880. .36143
Thote="L2 repeat: matches 2161. .2454 of consensus" 1715. .37752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .278 of consensus"
                                                            'note="AluJb repeat: matches 1. .295 of consensus"
                                                                                                /note="AluJb repeat: matches 1. .311 of consensus"
34637. .34708
                                                                                                                               note="Alu repeat: matches 244. .302 of consensus" 4882. .35177
                                                                                                                                                                                                                                                                                                                                                                                       consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 82. .152 of consensus"
1366. .41921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41825. .41894—
/note="15 copies 2 mer gg 65% conserved"
/note="18122
/note="MIR repeat: matches 82. .145 of consensus"
43974. .44086
/note="WIR repeat: matches 35. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46311. .46432
/note="MIR repeat: matches 35. .164 of consensus"
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9471. .39782
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                                                                                                                                                                                                                                                                                                                                                                                   note="AluJb repeat: matches 1. .309 of
                       . 209
10333. .30460
note="MER63A repeat: matches 78.
11898. .32190
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evidence=not_experimental
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15531. .45784
/note="AluJb repeat: matche
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Danio rerio
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; WP:, WORMDEP; Information on the WORMDEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chf6
RRI-90120 is from the library RPCI-I constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Homo sapiens clone RP11-20111, WORKING DRAFT SEQUENCE, 17 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPORTANT: This sequence is not the entire insert of clone RPI-90/20 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RPI-90/20 is at 1 in this sequence. The true left end of clone RPI-40E16 is at 173571 in this sequence. The true right end of clone RPII-420G6 is at 6201 in this sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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86.2%; Pred. No. 2.7e+02;
live 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Birren, B., Linton, L.; Nusbaum, (Homo sapiens, clone RP11-20111)
Unpublished
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
HOMO sapiens
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clone_lib="RPCI-1"
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AC013339/c
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                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission colly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL: Sw.; SWISSERCY; Tr.; TREMBL; Wp.; WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be enhanced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning dar were identified by Rick Waterman (Stephen Johnson lab, Washu). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-171P23
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Human DNA sequence from clone RP1-90J20 on chromosome 6p24.1-25.3,
complete sequence.
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Submitted (16-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquirles:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 18, 2001 this sequence version replaced gi:14041741.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
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Catarrhini; Hominidae; Homo.
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Pred. No. 2.7e+02;
0; Mismatches 4; Indels 0;
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                       Web site: http://www.sanger.ac.uk
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/db_xref="taxon:7955"
/clone="DKEY-171P23"
/clone_lib="DanioKey"
                                               Contact: zfish-help@sanger.ac.uk
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Mammalia, Eutheria, Primates,
1 (bases 1 to 173670)
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AL133351.34 GI:17907166
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Best Local Similarity 86.29
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NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Quality coverage: 6.0 in Q20 bases; sum-of-contigs
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B16 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 181522 bases at least Q40
Consensus quality: 185786 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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of 10826 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00 bp
f 14085 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 21318 bp in length
gap of 100 bp
contig of 24425 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11239 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16771 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10831 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 6717 bp in length gap of 100 bp contig of 5396 bp in length gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8917 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 183000; agarose-fp
Insert size: 187458; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
gap of 100
contig of
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gap of 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
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77.9%; Score 22.6; DB 2; Length 189058; 86.2%; Pred. No. 2.7e+02; 1ve 0; Mismatches 4; Indels 0;
5 148514: gap of 100 bp
5 189058: contig of 40544 bp in length.
Location/Qualifiers
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/clone lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                         3523. .16889
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23990. .148414
                                                                                                                                                                                                                                                                                                                                                                                             vector side:left"
16990. .23706
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                                                                                                                                                                                                                                                                                                                                                                                lone_end:SP6
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Matches 25; Conservative
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